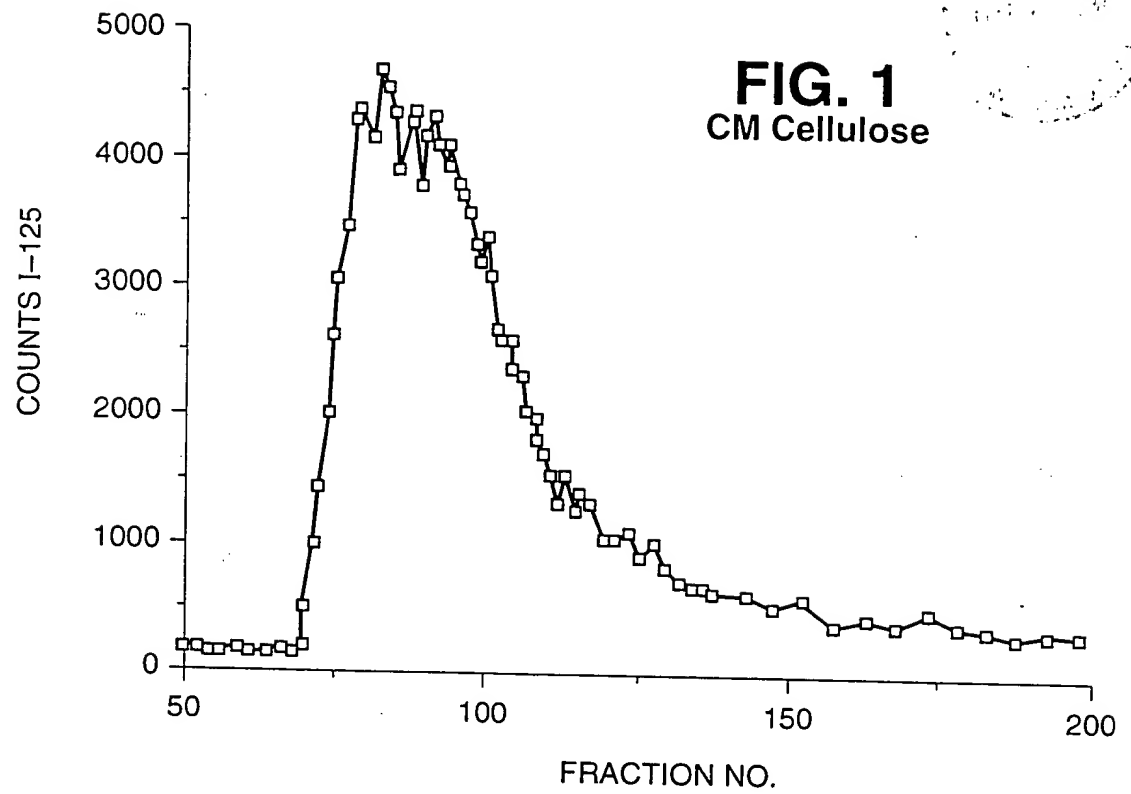
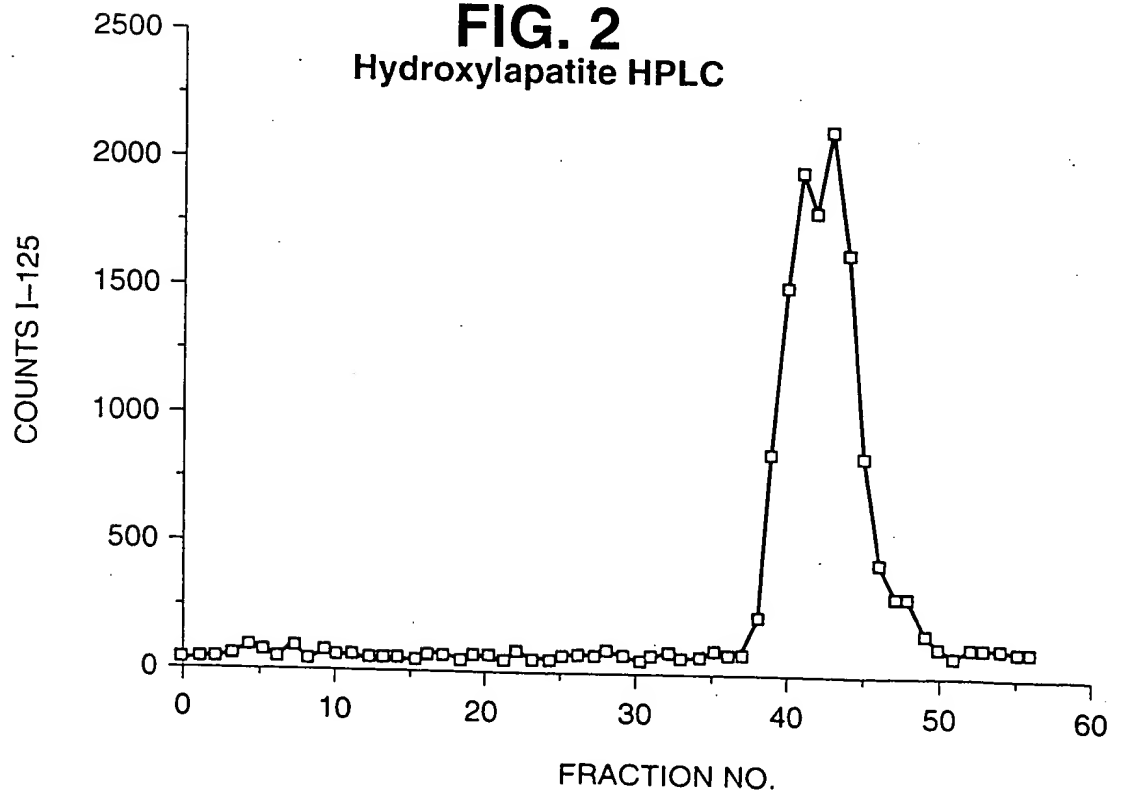
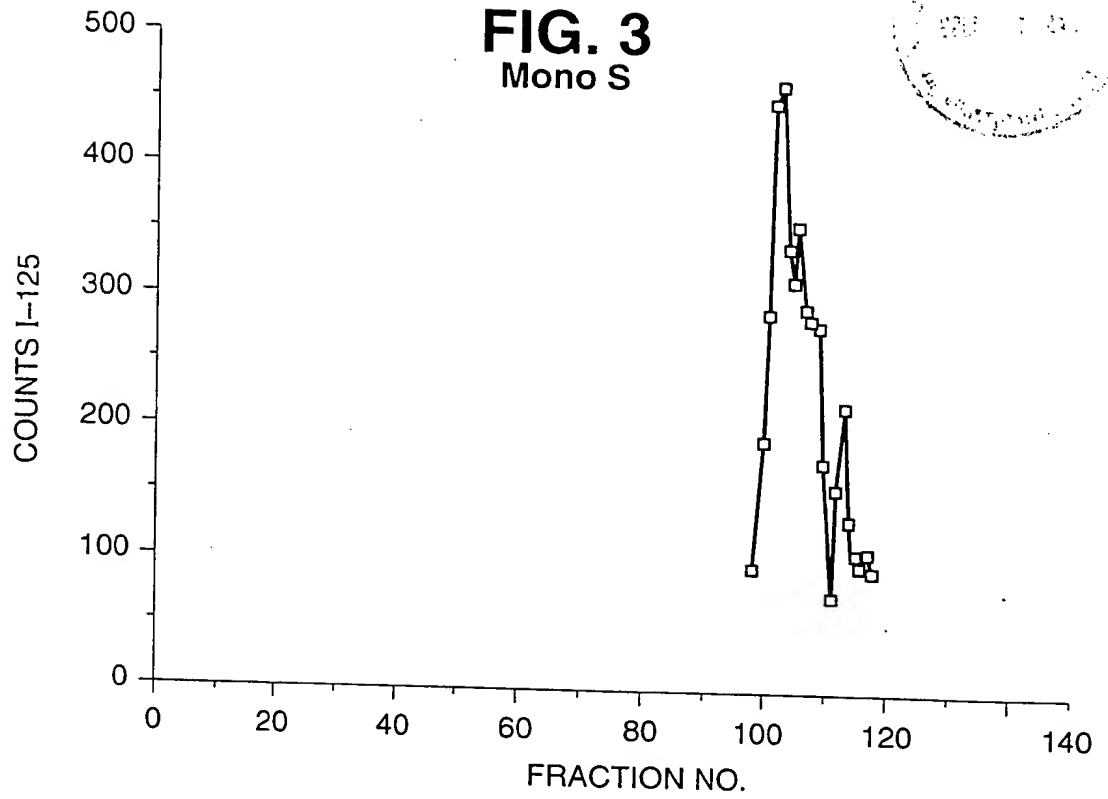


**FIG. 1**  
CM Cellulose**FIG. 2**  
Hydroxylapatite HPLC

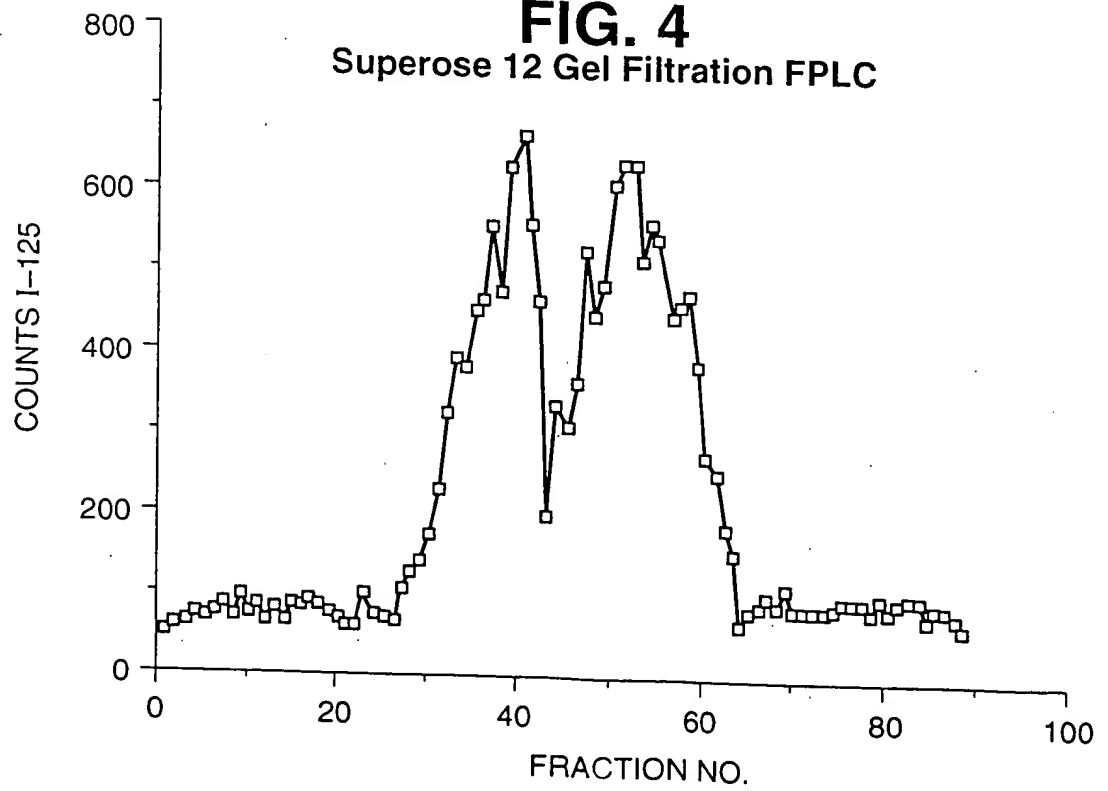
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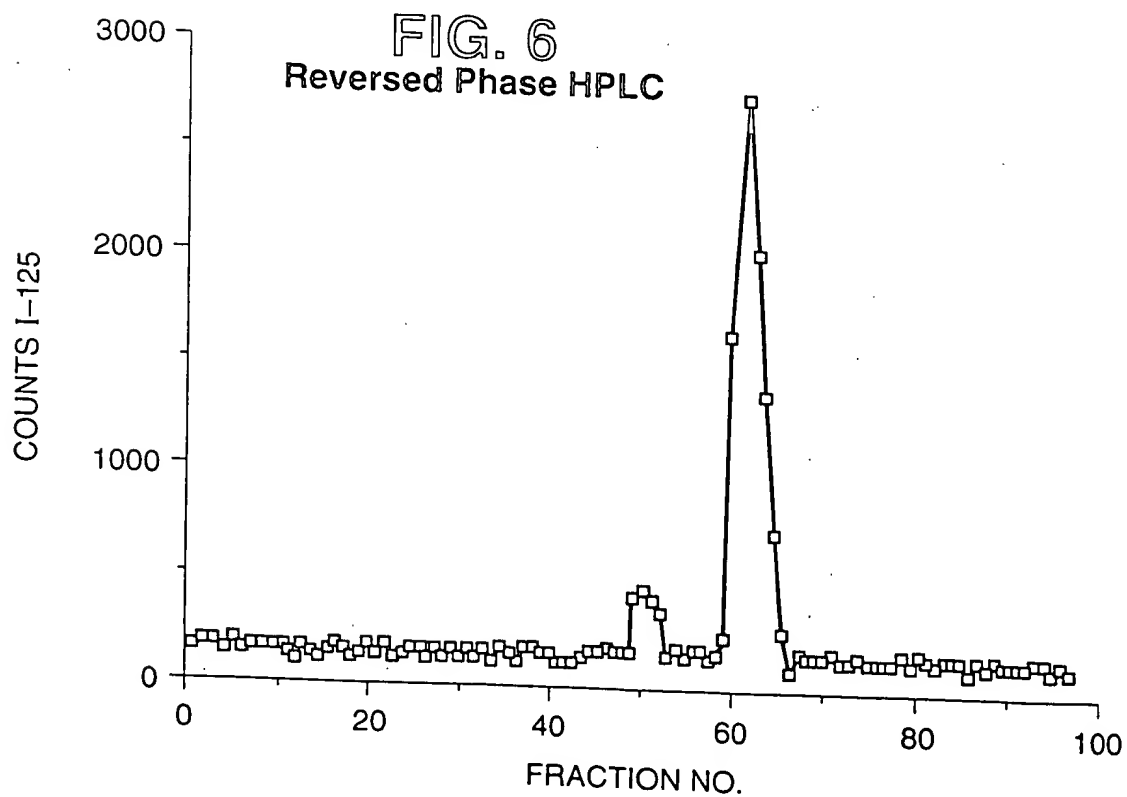
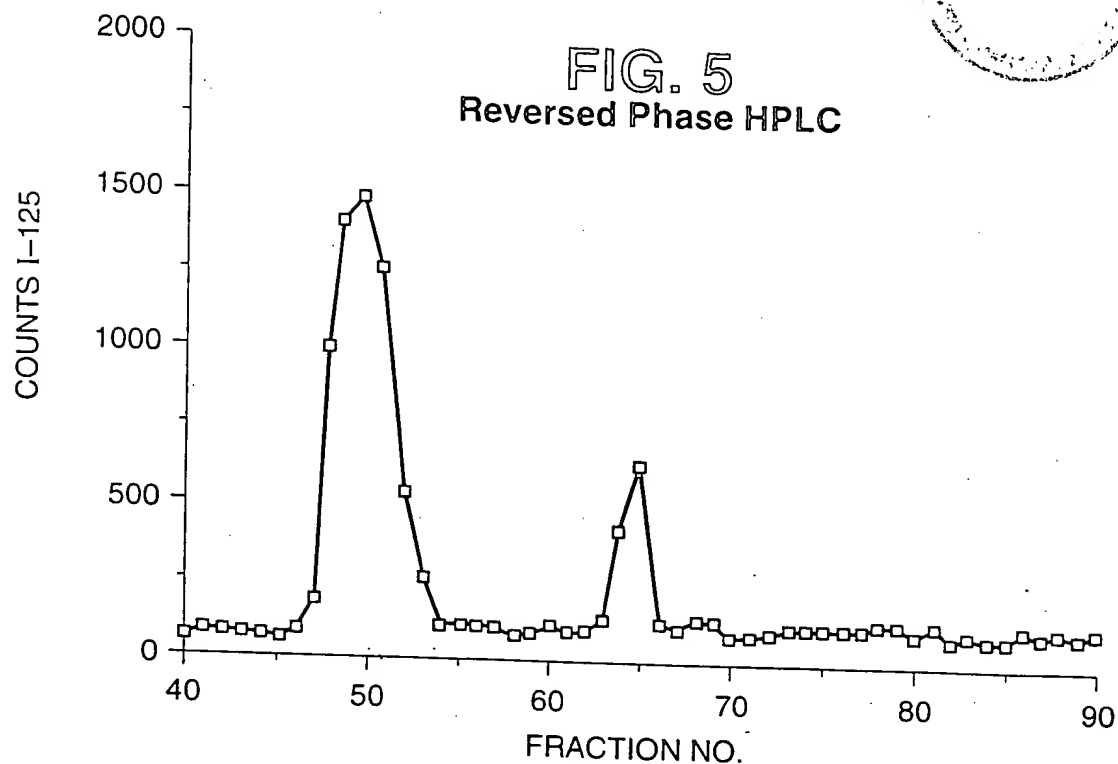
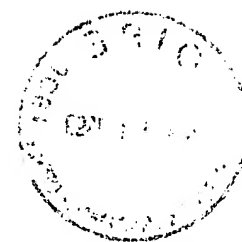


**FIG. 3**  
Mono S



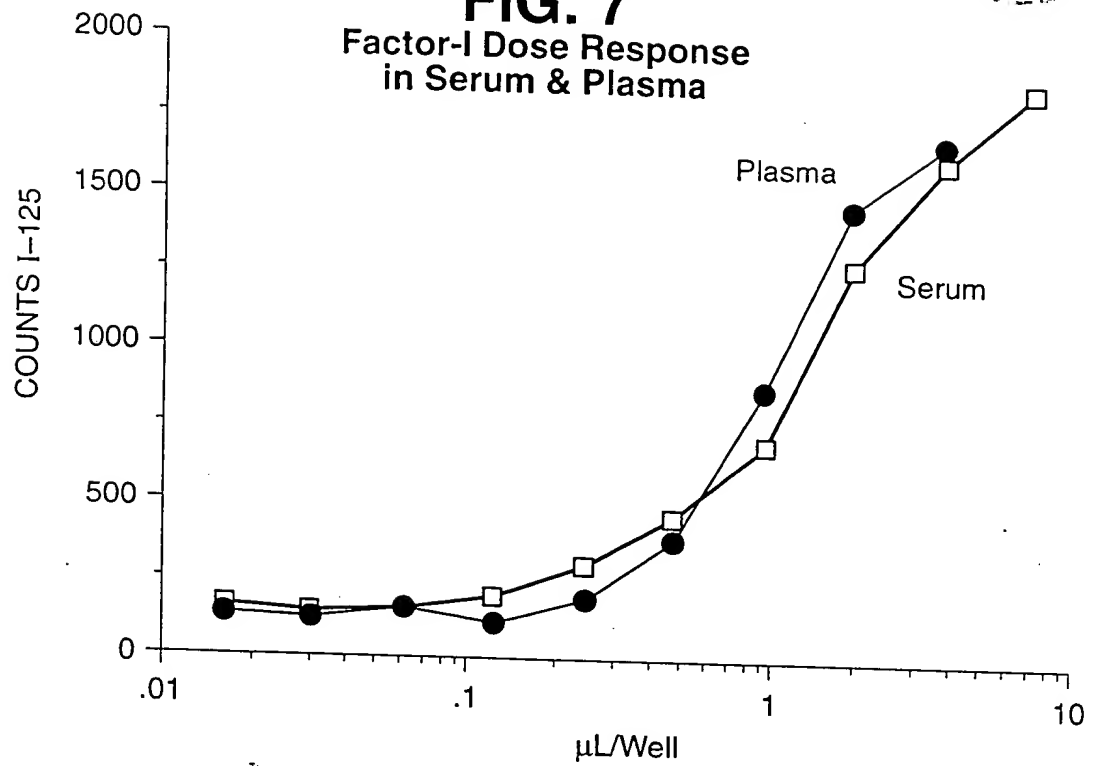
**FIG. 4**  
Superose 12 Gel Filtration FPLC



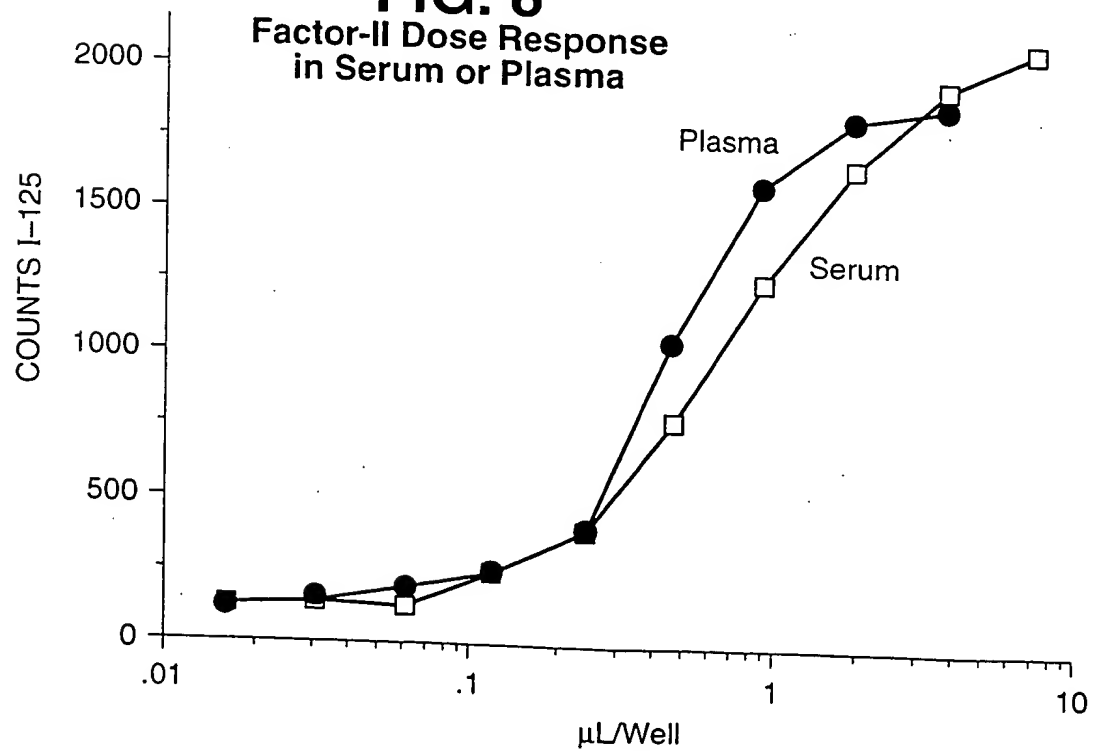




**FIG. 7**  
Factor-I Dose Response  
in Serum & Plasma



**FIG. 8**  
Factor-II Dose Response  
in Serum or Plasma



## FIG. 9

GGF-I 01	N-terminus F K G D A H T E	(SEQ ID NO: 1)	
GGF-I 02	Trypsin peptides K/R A S L A D E Y E Y M X K *	(SEQ ID NO: 2)	
GGF-I 03	K/R T E T S S G L X L K *	(SEQ ID NO: 3)	
GGF-I 04	K/R K L G E M W A E	(SEQ ID NO: 4)	HMG-1
GGF-I 05	K/R L G E K R A	(SEQ ID NO: 5)	HMG-1?
GGF-I 06	K/R I K S E H A G L S I G D T A K *	(SEQ ID NO: 6)	HMG-2
GGF-I 07	K/R A S L A D E Y E Y M R K *	(SEQ ID NO: 7)	
GGF-I 08	K/R I K G E H P G L S I G D V A K *	(SEQ ID NO: 8)	HMG-1
GGF-I 09	K/R M S E Y A F V Q T X R *	(SEQ ID NO: 9)	HMG-2
GGF-I 10	K/R S E H P G L S I G D T A K *	(SEQ ID NO: 10)	HMG-1
GGF-I 11	K/R A G Y F A E X A R *	(SEQ ID NO: 11)	
GGF-I 12	K/R K L E F L X A K *	(SEQ ID NO: 12)	
GGF-I 13	K/R T E M A S E Q G A	(SEQ ID NO: 13)	
GGF-I 14	K/R A K E A L A A L K *	(SEQ ID NO: 14)	
GGF-I 15	K/R F V L Q A K K *	(SEQ ID NO: 15)	
GGF-I 16	K/R L G E M W	(SEQ ID NO: 16)	HMG-1
GGF-I 17	Protease V8 peptides E T Q P D P G Q I L K K V P M V I G A Y T	(SEQ ID NO: 169)	
GGF-I 18	E Y K C L K F K W F K K A T V M	(SEQ ID NO: 17)	
GGF-I 19	E A K Y F S K X D A	(SEQ ID NO: 18)	LH-alpha
GGF-I 20	E X K F Y V P	(SEQ ID NO: 19)	
GGF-I 21	E L S F A S V R L P G C P P G V D P M V S F P V A L	(SEQ ID NO: 20)	LH-beta

# FIG. 10

10A

GGF-I 01	F K G D A H T E	(SEQ ID NO: 1)
GGF-I 02	A S L A D E Y E Y M X K	(SEQ ID NO: 22)
GGF-I 03	T E T S S S G L X L K	(SEQ ID NO: 23)
GGF-I 07	A S L A D E Y E Y M R K	(SEQ ID NO: 24)
GGF-I 11	A G Y F A E X A R	(SEQ ID NO: 25)
GGF-I 13	T T E M A S E Q G A	(SEQ ID NO: 26)
GGF-I 14	A K E A L A A L K	(SEQ ID NO: 27)
GGF-I 15	F V L Q A K K	(SEQ ID NO: 28)
GGF-I 17	E T Q P D P G Q I L K K V P M V I G A Y T	(SEQ ID NO: 29)
GGF-I 18	E Y K C L K F K W F K K A T V M	(SEQ ID NO: 17)

10B

GGF-I 20	E X K F Y V P	(SEQ ID NO: 19)
GGF-I 12	K L E F L X A K	(SEQ ID NO: 32)



FIG. 11

GGF-II 01	Trypsin peptides			(SEQ ID NO: 33)
GGF-II 02	K/R	V H Q V W A A K *		(SEQ ID NO: 34)
GGF-II 03	K/R	Y I F F M E P E A X S S G		(SEQ ID NO: 35)
GGF-II 04	K/R	L G A W G P P A F P V X Y		(SEQ ID NO: 36)
GGF-II 05	K/R	W F V V I E G K *		(SEQ ID NO: 164)
GGF-II 06	K/R	A L A A A G Y D V E K *	Histone H1	(SEQ ID NO: 165)
GGF-II 07	K/R	L V L R *		(SEQ ID NO: 166)
GGF-II 08	K/R	X X Y P G Q I T S N	Trypsin	(SEQ ID NO: 37)
GGF-II 09	K/R	A S P V S V G S V Q E L V Q R *		(SEQ ID NO: 38)
GGF-II 10	K/R	V C L L T V A A P P T		(SEQ ID NO: 39)
	K/R	D L L L X V		
GGF-II 11	Lysyl Endopeptidase-C peptides			(SEQ ID NO: 51)
GGF-II 12	K	V H Q V W A A K *		(SEQ ID NO: 52)
	K	A S L A D S G E Y M X K *		





# FIG. 12

A

GGF-II 01	V H Q V W A A K	(SEQ ID NO: 45)
GGF-II 02	Y I F F M E P E A X S S G	(SEQ ID NO: 46)
GGF-II 03	L G A W G P P A F P V X Y	(SEQ ID NO: 47)
GGF-II 04	W F V V I E G K	(SEQ ID NO: 48)
GGF-II 08	A S P V S V G S V Q E L V Q R	(SEQ ID NO: 49)
GGF-II 09	V C L L T V A A P P T	(SEQ ID NO: 50)
GGF-II 11	K V H Q V W A A K	(SEQ ID NO: 51)
GGF-II 12	K A S L A D S G E Y M X K	(SEQ ID NO: 52)

B

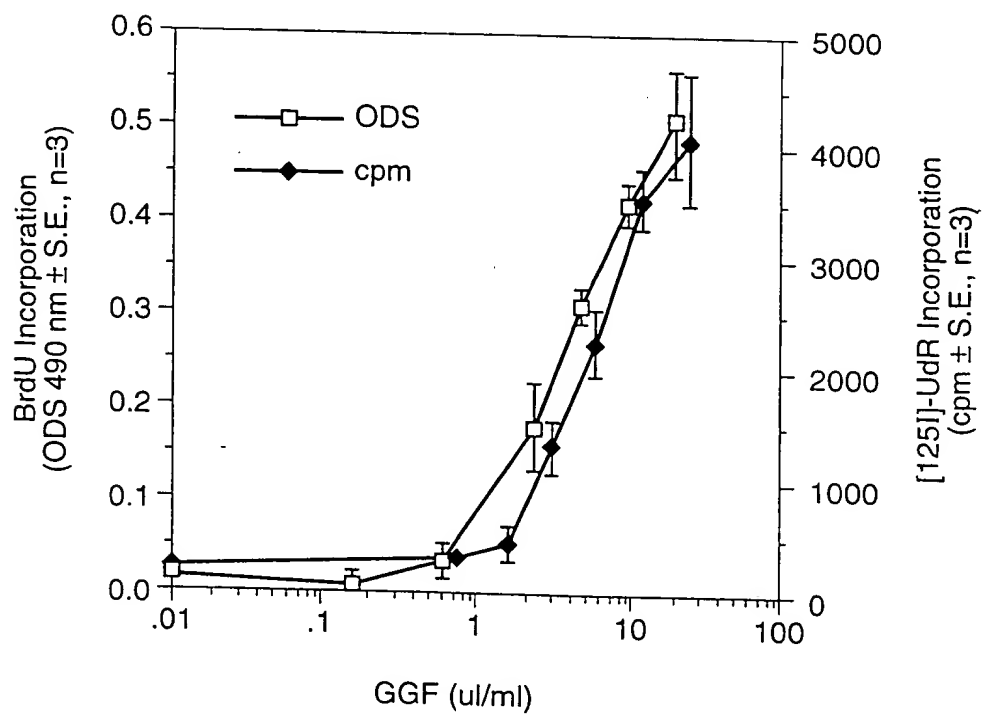
Novel Factor II Peptides - others

GGF-II 10	D L L L X V	(SEQ ID NO: 53)
-----------	-------------	-----------------



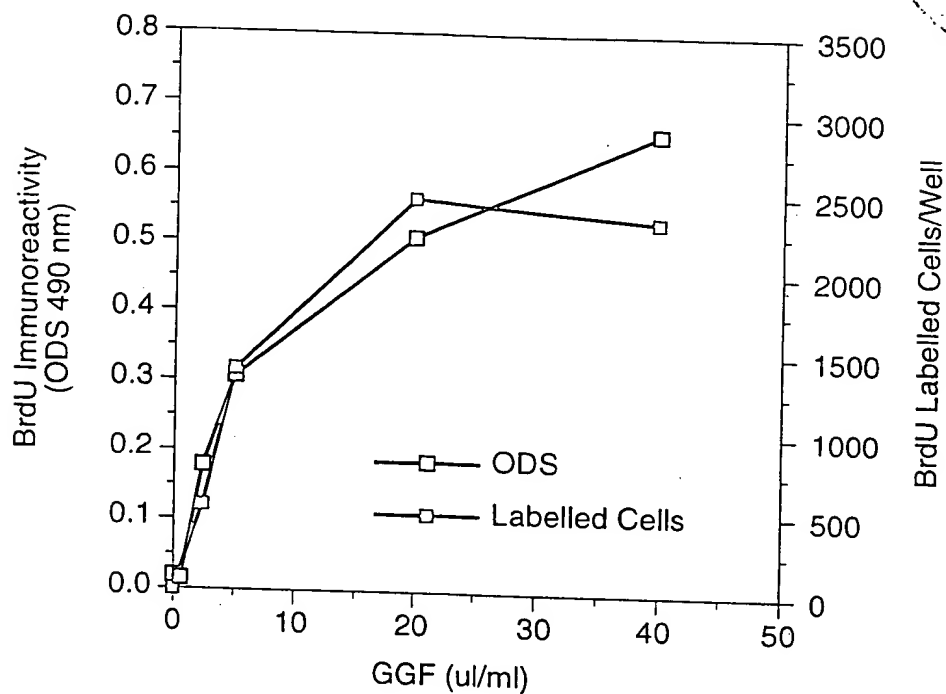


**FIG. 13**  
Comparison of BrdU-ELISA and [ $^{125}$ I]UdR Counting Method for  
the DNA Synthesis Assay in Schwann Cell Cultures

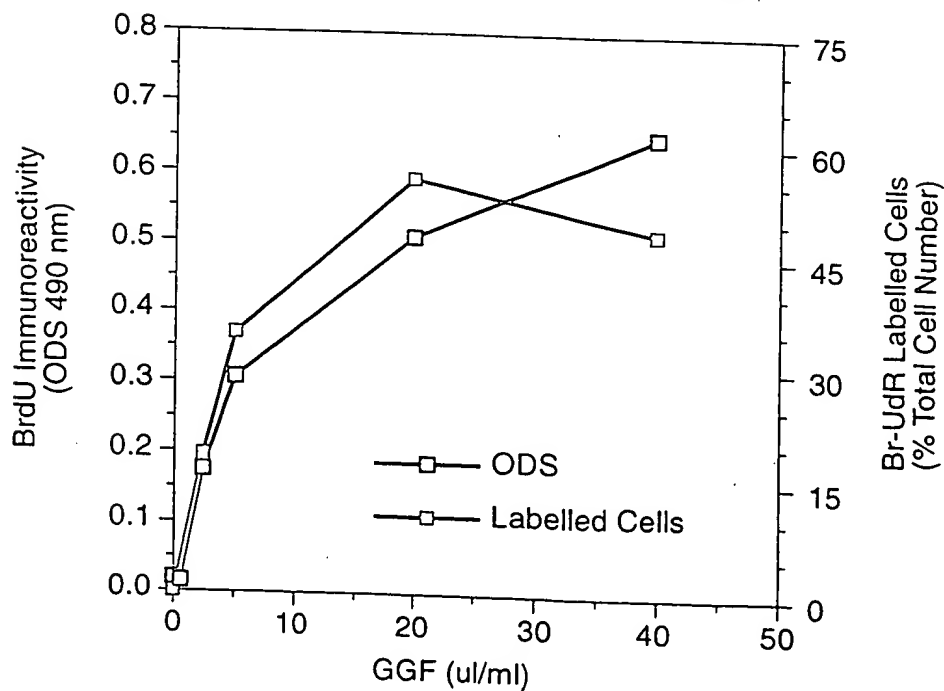


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**FIG. 14A**  
Comparison of Br-UdR Immunoreactivity  
and Br-UdR Labelled Cell Number



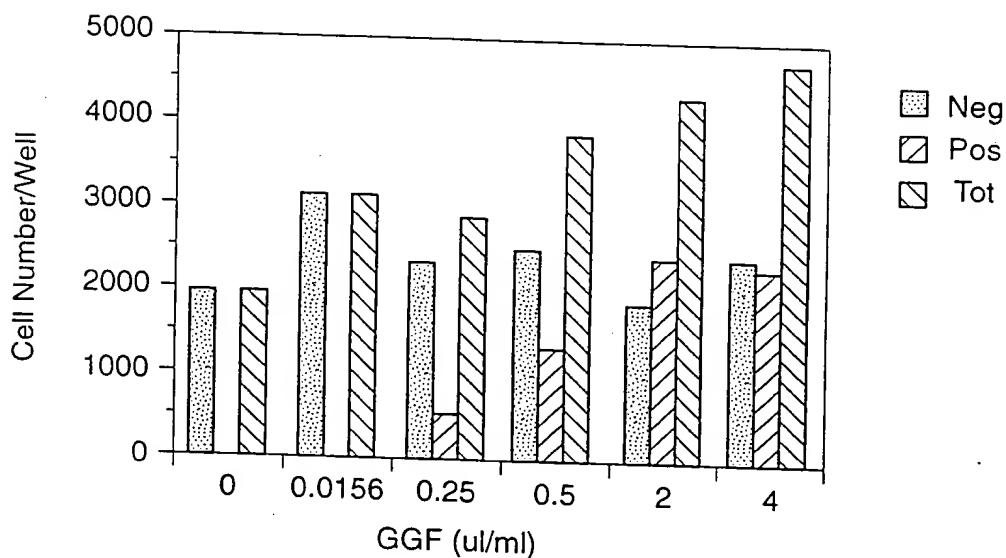
**FIG. 14B**  
Comparison of Br-UdR Immunoreactivity  
and Br-UdR Labelled Cell Number



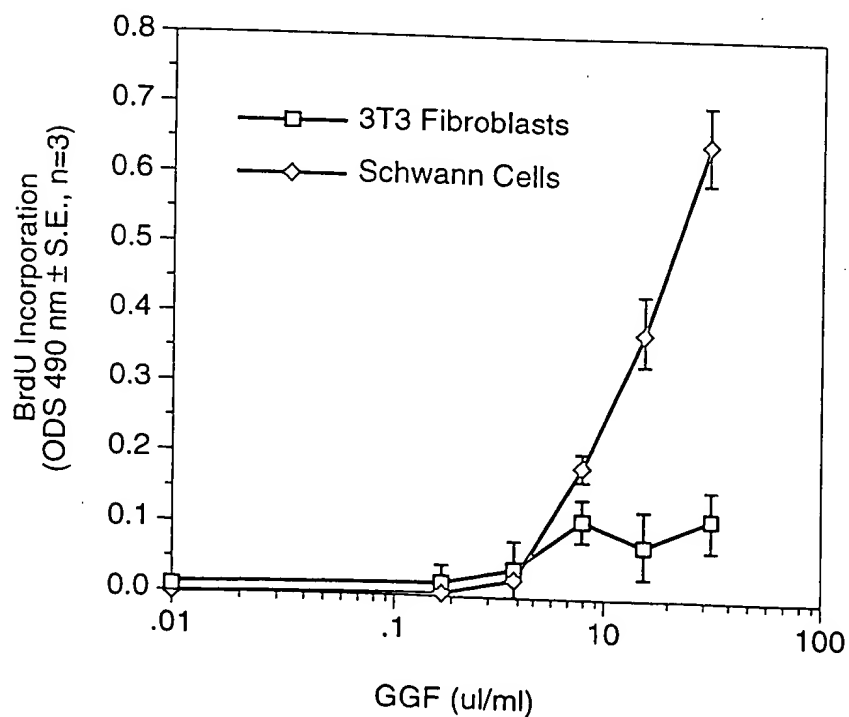
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**FIG. 15**  
Mitogenic Response of Rat Sciatic Nerve Schwann cell to GGFs

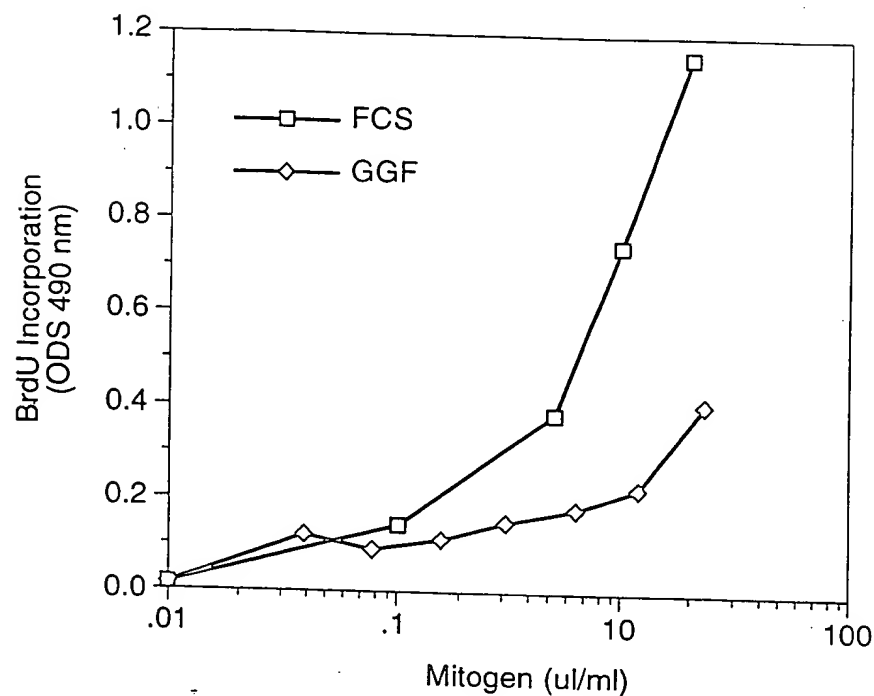


**FIG. 16**  
DNA Synthesis in Rat Sciatic Nerve Schwann Cells and 3T3 Fibroblasts in the presence of GGFs

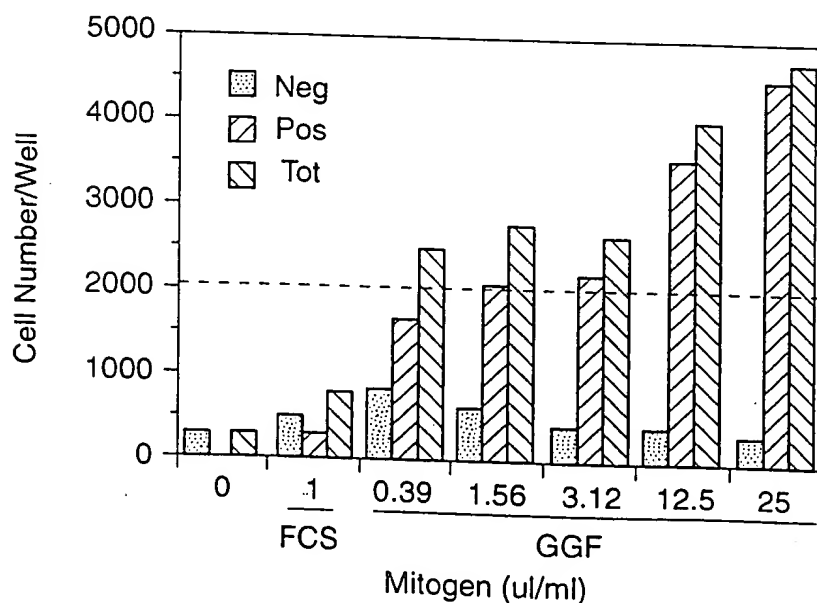


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**FIG. 17**  
**Mitogenic Response of**  
**BHK 21 C13 Cells to FCS and GGFs**



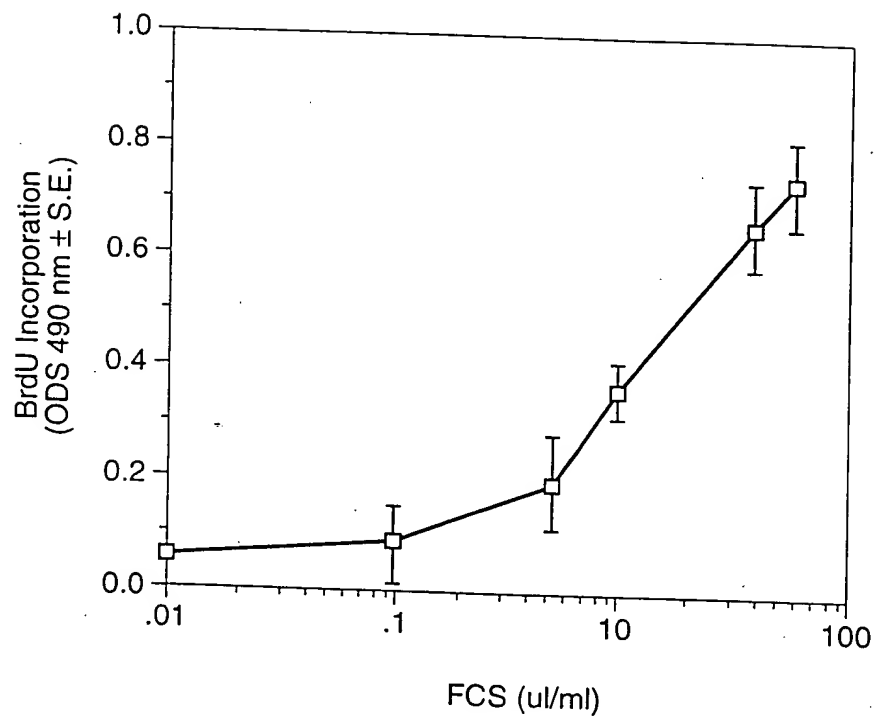
**FIG. 18**  
**Survival and Proliferation of BHK21 C13 Cell**  
**Microcultures After 48 Hours in Presence of GGFs**



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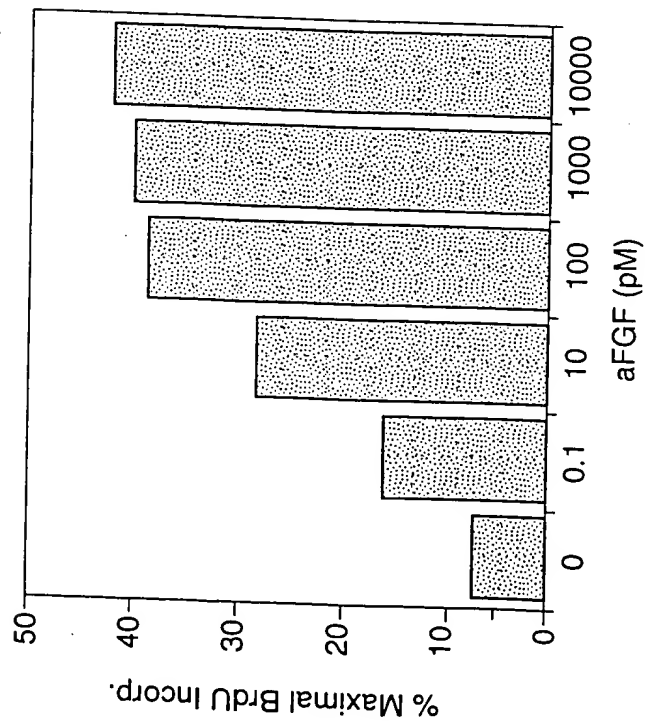


**FIG. 19**  
Mitogenic Response  
of C6 Cells to FCS

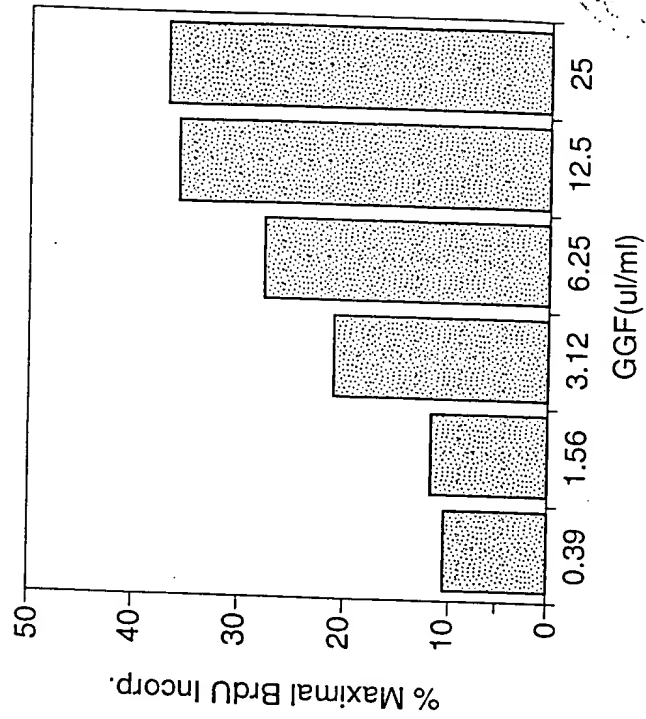




**FIG. 20A**  
Mitogenic Response of  
C6 Cells to aFGF & GGFs



**FIG. 20B**  
Mitogenic Response of  
C6 Cells to aFGF & GGFs





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## FIG. 21

## Degenerate Oligonucleotide Probes for Factor I &amp; Factor II

Oligo	Sequence	Peptide	
535	TTYAARGGNGAYGCNCAYAC!	GGFI-1	(SEQ ID NO: 54)
536	CATRTAYTCRTAYTCRTCNGC!	GGFI-2	(SEQ ID NO: 55)
537	TGYTCNGANGCCATYTCNGT!	GGFI-13	(SEQ ID NO: 56)
538	TGYTCRCTNGCCATYTCNGT!	GGFI-13	(SEQ ID NO: 57)
539	CCDATNACCATNGGNACYTT!	GGFI-17	(SEQ ID NO: 58)
540	GCNGCCCANACYTGRTGNAC!	GGFII-1	(SEQ ID NO: 59)
541	GCYTCNGGYTCCATRAARAA!	GGFII-2	(SEQ ID NO: 60)
542	CCYTCDATNACNACRAACCA!	GGFII-4	(SEQ ID NO: 61)
543	TCNGCRAARTANCCNGC!	GGFI-11	(SEQ ID NO: 62)
544	GCNGCNAGNGCYTCYTTNGC!	GGFI-14	(SEQ ID NO: 63)
545	GCNGCYAANGCYTCYTTNGC!	GGFI-14	(SEQ ID NO: 64)
546	TTYTTNGCYTGNAGNACRAA!	GGFI-15	(SEQ ID NO: 65)
551	TTYTTNGCYTGYAANACRAA!	GGFI-15	(SEQ ID NO: 66)
568	TGNACNAGYTCYTGAC!	GGFII-8	(SEQ ID NO: 67)
569	TGNACYAAYTCYTGAC!	GGFII-8	(SEQ ID NO: 68)
609	CATRTAYTCNCCNGARTCNGC!	GGFII-12	(SEQ ID NO: 69)
610	CATRTAYTCNCCRCTRTCNGC!	GGFII-12	(SEQ ID NO: 70)
649	NGARTCNGCYAANGANGCYTT!	GGFII-12	(SEQ ID NO: 71)
650	NGARTCNGCNAGNGANGCYTT!	GGFII-12	(SEQ ID NO: 72)
651	RCTRTCNGCYAANGANGCYTT!	GGFII-12	(SEQ ID NO: 73)
652	RCTRTCNGCNAGNGANGCYTT!	GGFII-12	(SEQ ID NO: 74)
653	NGARTCNGCYAARCTNGCYTT!	GGFII-12	(SEQ ID NO: 75)
654	NGARTCNGCNAGRCTNGCYTT!	GGFII-12	(SEQ ID NO: 76)
655	RCTRTCNGCYAARCTNGCYTT!	GGFII-12	(SEQ ID NO: 78)
656	RCTRTCNGCNAGRCTNGCYTT!	GGFII-12	(SEQ ID NO: 79)
659	ACNACNGARATGGCTCNGA!	GGFI-13	(SEQ ID NO: 80)
660	ACNACNGARATGGCAGYNGA!	GGFI-13	(SEQ ID NO: 81)
661	CAYCARGTNTGGGCNGCNAA!	GGFII-1	(SEQ ID NO: 82)
662	TTYGTNGTNAHARGGNAA!	GGFII-4	(SEQ ID NO: 83)
663	AARGGNGAYGCNCAYACNGA!	GGFI-1	(SEQ ID NO: 84)
664	GARGCNYTNGCNGCNYTNAA!	GGDI-14	(SEQ ID NO: 85)
665	GTNGGNTCNGTNCARGARYT!	GGFII-8	(SEQ ID NO: 86)
666	GTNGGNAGYGTNCARGARYT!	GGFII-8	(SEQ ID NO: 87)
694	NACYTTYTTNARHATYTGACC!	GGFI-17	(SEQ ID NO: 88)

# FIG. 22

## Putative Bovine Factor II Gene Sequences

SEQ ID NO: 89:

TCTAA AAC TAC AGA GAC TGT ATT TTC ATG ATC ATA GTT CTG TGA AAT ATA Asn Tyr Arg Asp Cys Ile Phe Met Ile Ile Val Leu Xaa Asn Ile	53
CTT AAA CCG CTT TGG TCC TGA TCT TGT AGG AAG TCA GAA CTT CGC ATT Leu Lys Pro Leu Trp Ser Xaa Ser Cys Arg Lys Ser Glu Leu Arg Ile	101
AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Ser Met Cys Lys Val Ile	149
AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Arg Ile Val Glu	197
TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA Ser Asn Gly Lys Arg Cys Leu Leu Arg Ala Ile Ser Gln Ser Leu Arg	245
GGA GTG ATC AAG GTA TGT GGT CAC ACT TGA ATC ACG CAG GTG TGT GAA Gly Val Ile Lys Val Cys Gly His Thr Xaa Ile Thr Gln Val Cys Glu	293
ATC TCA TTG TGA ACA AAT AAA AAT CAT GAA AGG AAA ACT CTA TGT TTG Ile Ser Cys Xaa Thr Asn Lys Asn His Glu Arg Lys Thr Leu Cys Leu	341
AAA TAT CTT ATG GGT CCT CCT GTA AAG CTC TTC ACT CCA TAA GGT GAA Lys Tyr Leu Met Gly Pro Pro Val Lys Leu Phe Thr Pro Xaa Gly Glu	389
ATA GAC CTG AAA TAT ATA TAG ATT ATT T Ile Asp Leu Lys Tyr Ile Xaa Ile Ile	417



# FIG. 23A

## PCR Primers for Factor I & Factor II

### Degenerate PCR Primers

Oligo Sequence	Peptide	(SEQ ID NO: 90)
657 CCGAATTCTGCAGGARACNCARCCNGAYCCNGG!	GGFI-17	(SEQ ID NO: 90)
658 AAGGATCCTGCAGNGTRTANGCNCCHATNACCATNGG!	GGFI-17	(SEQ ID NO: 91)
667 CCGAATTCTGCAGGCNGAYTCNGGNGARTAYATG!	GGFII-12	(SEQ ID NO: 92)
668 CCGAATTCTGCAGGCNGAYATYGGNGARTAYAT!	GGFII-12	(SEQ ID NO: 93)
669 AAGGATCCTGCAGNNNCATRTAYTCNCCNGARTC!	GGFII-12	(SEQ ID NO: 94)
670 AAGGATCCTGCAGNNNCATRTAYTCNCCRRTRTC!	GGFII-12	(SEQ ID NO: 95)
671 CCGAATTCTGCAGCAYCARGTNTGGCNGCNA!	GGFII-1	(SEQ ID NO: 96)
672 CCGAATTCTGCAGATRTTYTAYTGARCCNGARG!	GGFII-2	(SEQ ID NO: 97)
673 CCGAATTCTGCAGGGGCCNCCNGCNTTYCCNGT!	GGFII-3	(SEQ ID NO: 98)
674 CCGAATTCTGCAGTGGTTYGTNGTNATHGARGG!	GGFII-4	(SEQ ID NO: 99)
677 AAGGATCCTGCAGYTTNGCNGCCCANACYTGRTG!	GGFII-1	(SEQ ID NO: 100)
678 AAGGATCCTGCAGGCYTCNGGYTCCATRAA!	GGFII-2	(SEQ ID NO: 101)
679 AAGGATCCTGCAGACNGGGAANGCNGGNGNCC!	GGFII-3	(SEQ ID NO: 102)
680 AAGGATCCTGCAGYTTNCCYTCDATNACNACRAAC!	GGFII-4	(SEQ ID NO: 103)
681 CATRTAYTCRTAYTCTCNGCAAGGATCCTGCAG!	GGFI-2	(SEQ ID NO: 104)
682 CCGAATTCTGCAGAAARGNGAYGCNCAACNGA!	GGFI-1	(SEQ ID NO: 105)
683 GCNGCYAANGCYRCYTTNGCAAGGATCCTGCAG!	GGFI-14	(SEQ ID NO: 106)
684 GCNGCNAGNGCYTCYTTNGCAAGGATCCTGCAG!	GGFI-14	(SEQ ID NO: 107)
685 TCNGCRAARTANCCNGCAAGGATCCTGCAG!	GGFII-1	(SEQ ID NO: 108)

# FIG. 23B

## PCR Primers for Factor I & Factor II

### Unique PCR Primers for Factor II

Oligo Sequence	Comment	(SEQ ID NO: 109)
711 CATCGATCTGCAGGCTGATTCGGAGATATATGTGCA!	3' RACE	(SEQ ID NO: 110)
712 AAGGATCCTGCAGCCACATCTCGAGTCGACATCGATT!	3' RACE	(SEQ ID NO: 111)
713 CCGAATTCTGCAGTGATCAGCAAACTAGGAAATGACA!	5' RACE	(SEQ ID NO: 112)
721 CATCGATCTGCAGCCTAGTTTGCTGATCACTTTGCAC!	5' RACE; ANCHORED	(SEQ ID NO: 113)
722 AAGGATCCTGCAGTATATTTCTCCAGAAATCAGCCAGTG!	EXON A	(SEQ ID NO: 114)
725 AAGGATCCTGCAGGCACGCACTTCGCATTCCTTA!	EXON A	(SEQ ID NO: 115)
726 CCGAATTCTGCAGCAGAACTTCGCATTAGCAAAGC!	EXONS B+A	(SEQ ID NO: 116)
771 CATCCCGGATGAAGAGTCAGGAGTCTGTGGCA!	ANCHORED	(SEQ ID NO: 117)
772 ATACCCGGGCTGCAGACAATGAGATTTACACACCTGCG!	EXONS B+A	(SEQ ID NO: 118)
773 AAGGATCCTGCAGTTTGGAACTTCCACAGACTCCT!		(SEQ ID NO: 119)
776 ATACCCGGGCTGCAGATGAGATTTACACACCTGCGTGA!		

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**FIG. 24**  
**Summary of Contiguous GGF-II**  
**cDNA Structures & Sequences**

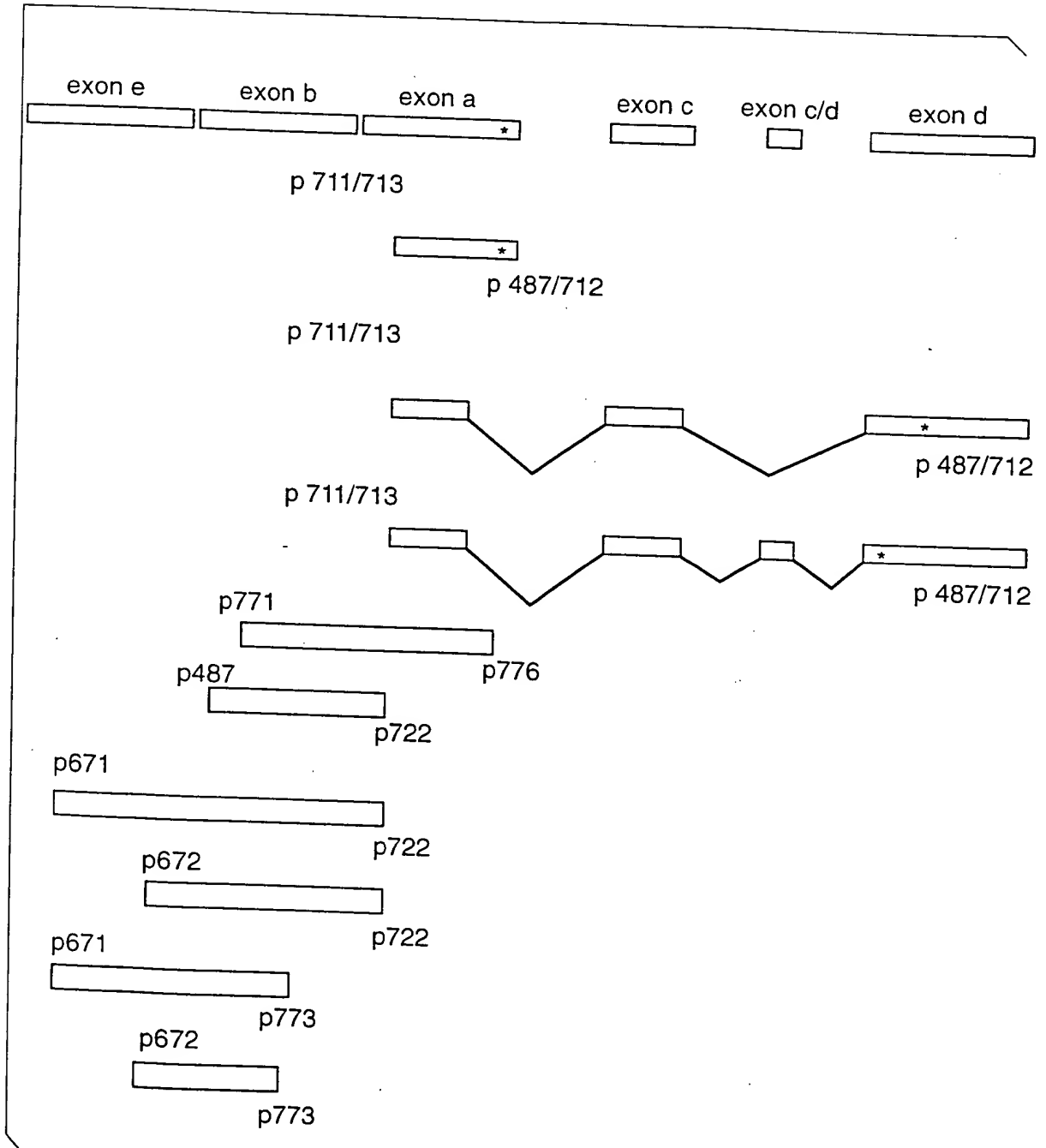


FIG. 25

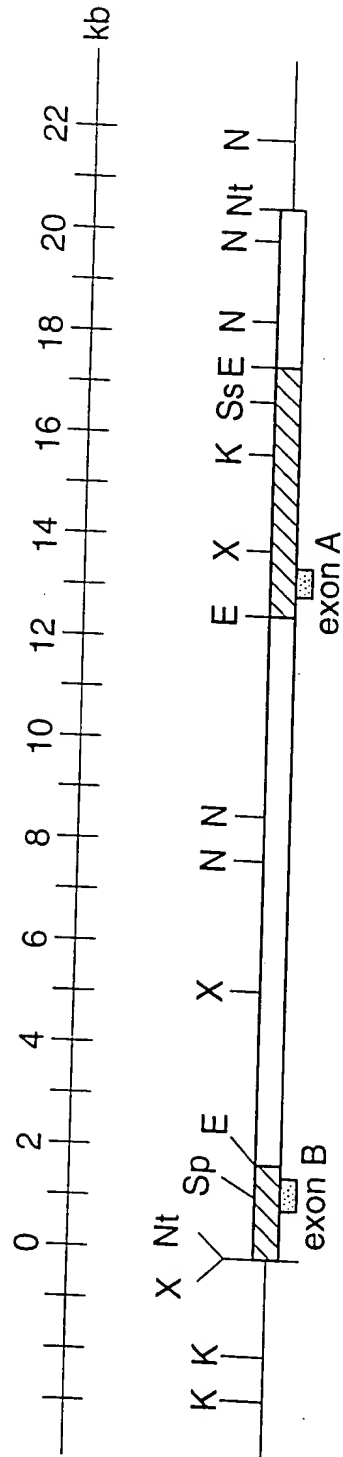
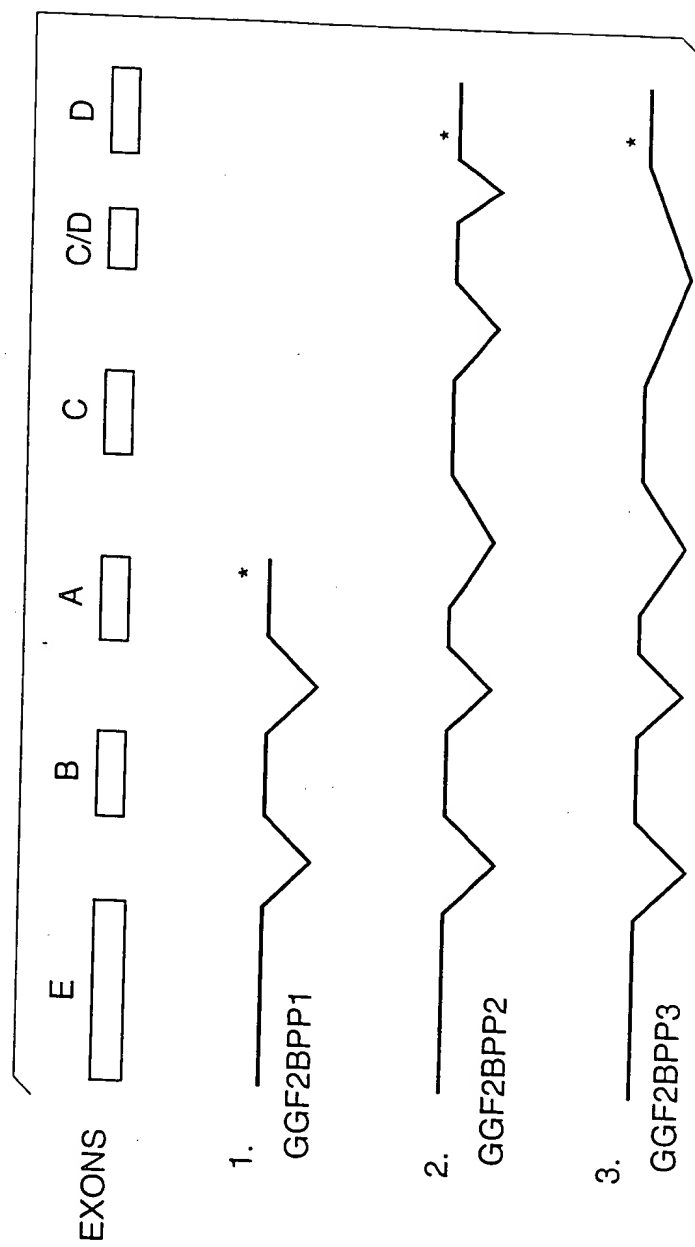


FIG. 26  
Alternative Gene Products of Putative Bovine GGF-II



**FIG. 27**

**GGF-II Peptides Identified in Deduced Amino Acid  
Sequences of Putative Bovine GGF-II Proteins**

Peptide	Pos.	Sequence match	ID Sequences
II-1	1:	VHQVWAAK HQVWAAK AAGLK	(SEQ ID NO:120)
II-10	14:	DLLLXV GGLKK dslltv RLGAW	(SEQ ID NO:121)
II-03	21:	LGAWGPPAFPVXY LLTVR lgawghpafpscgl RLKED	(SEQ ID NO:122) (SEQ ID NO:123)
II-02	41:	YIFFMEPEAXSSG KEDSR YIFFMEPEANSSG GPGRL	(SEQ ID NO:124) (SEQ ID NO:125)
II-6	103:	LVLR VAGSK LVLR CETSS	(SEQ ID NO:126)
I-18	112:	EYKCLKFKWFKKATVM CETSS eysslkfkfwkngsel SRKNK	(SEQ ID NO:127) (SEQ ID NO:128)
II-12	151:	KASLADSGEYMXK ELRIS KASLADSGEYMCK VISKL	(SEQ ID NO:129) (SEQ ID NO:130)
I-07	152:	ASLADEYEYMRK LRISK asladsgeymck VISKL	(SEQ ID NO:131) (SEQ ID NO:132)

# FIG. 28A

SEQ ID NO: 133:

CCTGCAG CAT CAA GTG TGG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG 55  
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu

CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GGC TTC CCC TCC TGC 103  
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys

GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG 151  
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu

GCC AAC AGC AGC GGC GGC CCC GGC CTT CCG AGC CTC CTT CCC CCC 199  
Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro

TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG 247  
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val

CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG 295  
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu

TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA 343  
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu

TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC 391  
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG 439  
Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys

TCA GAA CTT CGC ATT AGC AAA CCG TCA CTG GCT GAT TCT GGA GAA TAT 487  
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC 535  
Met Cys Lys Val Ile Ser Lys Leu Gly Lys Asn Asp Ser Ala Ser Ala Asn

ATC ACC ATT GTG GAG TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT 583  
Ile Thr Ile Val Glu Ser Asn Gly Lys Arg Cys Leu Leu Arg Ala Ile

TCT CAG TCT CTA AGA GGA GTG ATC AAG GTA TGT GGT CAC ACT 625  
Ser Gln Ser Leu Arg Gly Val Ile Lys Val Cys Gly His Thr

TGAATCACGC AGGTGTGTGA AATCTCATTTG TGAACAAATA AAAATCATGA AAGGAAAAA 685  
AAAAAATAA AATCGATGTC GACTCGAGAT GTGGCTGCAG GTCGACTCTA GAGGATCCC 744

# FIG. 28B

## Nucleotide Sequences & Deduced Amino Acid Sequences of GGF2BPPP2

SEQ ID NO: 134:

CCTGCAG	CAT	CAA	GTG	TGG	GCG	GCG	AAA	GCC	GGG	GGC	TTG	AAG	AAG	GAC	TCG	CTG	55
	His	Gln	Val	Trp	Ala	Ala	Lys	Ala	Gly	Gly	Leu	Lys	Lys	Asp	Ser	Leu	
CTC	ACC	GTG	CGC	CTG	GGC	GCC	TGG	GGC	CAC	CCC	GCC	TTC	CCC	TCC	TGC		103
Leu	Thr	Val	Arg	Leu	Gly	Ala	Trp	Gly	His	Pro	Ala	Phe	Pro	Ser	Cys		
GGG	CGC	CTC	AAG	GAG	GAC	AGC	AGG	TAC	ATC	TTC	TTC	ATG	GAG	CCC	GAG		151
Gly	Arg	Leu	Lys	Glu	Asp	Ser	Arg	Tyr	Ile	Phe	Phe	Met	Glu	Pro	Glu		
GCC	AAC	AGC	AGC	GGC	GGG	CCC	GGC	CGC	CTT	CCG	AGC	CTC	CTT	CCC	CCC		199
Ala	Lys	Ser	Ser	Gly	Gly	Pro	Gly	Arg	Leu	Pro	Ser	Leu	Leu	Pro	Pro		
TCT	CGA	GAC	GGG	CCG	GAA	CCT	CAA	GAA	GGT	CAG	CCG	GGT	GCT	GTG			247
Ser	Arg	Asp	Gly	Pro	Glu	Pro	Gln	Glu	Gly	Gln	Pro	Gly	Ala	Val			
CAA	CGG	TGC	GCC	TTG	CCT	CCC	CGC	TTG	AAA	GAG	ATG	AAG	AGT	CAG	GAG		295
Gln	Arg	Cys	Ala	Leu	Pro	Pro	Arg	Leu	Lys	Glu	Met	Lys	Ser	Gln	Glu		
TCT	GTG	GCA	GGT	TCC	AAA	CTA	GTG	CTT	CGG	TGC	GAG	ACC	AGT	TCT	GAA		343
Ser	Val	Ala	Gly	Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	Ser	Ser	Glu		
TAC	TCC	TCT	CTC	AAG	TTC	AAG	TGG	TTC	AAG	AAT	GGG	AGT	GAA	TTA	AGC		391
Tyr	Ser	Ser	Leu	Lys	Phe	Lys	Trp	Phe	Lys	Asn	Gly	Ser	Glu	Leu	Ser		
CGA	AAG	AAC	AAA	CCA	GAA	AAC	ATC	AAG	ATA	CAG	AAA	AGG	CCG	GGG	AAG		439
Arg	Lys	Asn	Lys	Gly	Gly	Asn	Ile	Lys	Ile	Gln	Lys	Arg	Pro	Gly	Lys		
TCA	GAA	CTT	CGC	ATT	AGC	AAA	GCG	TCA	CTG	GCT	GAT	TCT	GGA	GAA	TAT		487
Ser	Glu	Leu	Arg	Ile	Ser	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly	Glu	Tyr		
ATG	TGC	AAA	GTG	ATC	AGC	AAA	CTA	GGA	AAT	GAC	AGT	GCC	TCT	GCC	AAC		535
Met	Cys	Lys	Val	Ile	Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	Ala	Asn		



**FIG. 28C**  
**Nucleotide Sequences & Deduced Amino Acid Sequences of GG2BPP2**

ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr	583
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT Ser His Leu Val Lys Ser Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	631
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	679
TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn	727
GTG CCC ATG AAA GTC CAA ACC CAA GAA AGT GCC CAA ATG AGT TTA CTG Val Pro Met Lys Val Gln Thr Gln Glu Ser Ala Gln Met Ser Leu Leu	775
GTG ATC GCT GCC AAA ACT ACG TAATGGCCAG CTTCTACAGT ACGTCCACTC Val Ile Ala Ala Lys Thr Thr	826
CCTTTCTGTC TCTGCCTGAA TAGCGCATCT CAGTCGGTGC CGCTTCTTG TTGCCGCATC	886
TCCCCCTCAGA TTCCTCCTAG AGCTAGATGC GTTTACCAG GTCTAACATT GACTGCCCTCT	946
GCCTGTGCGA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCTCTGTC CGTGACTAGT	1006
GGGCTCTGAG CTACTCGTAG GTGCGTAAGG CTCCAGTGTT TCTGAAATTG ATCTTGAATT	1066
ACTGTGATAC GACATGATAG TCCCTCTCAC CCAGTGCAAT GACAATAAAG GCCTTGAAAA	1126
GTCAAAAAAA AAAAAAATAA AAAAAATCGA TGTCGACTCG AGATGTGGCT GCAGGTCGAC	1186
TCTAGAG	1193

# FIG. 28D

## Nucleotide Sequences & Deduced Amino Acid Sequences of GGF2BPP3

SEQ ID NO: 135:

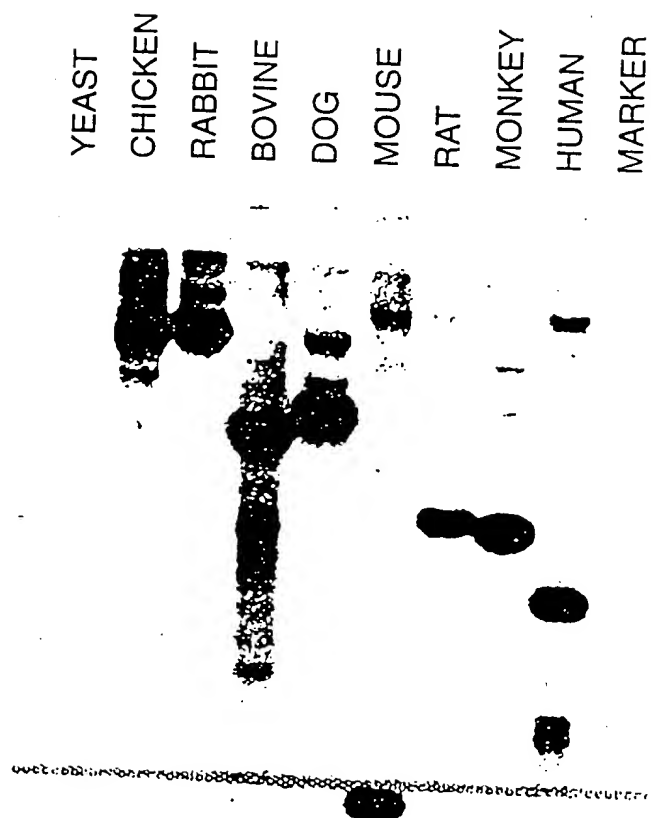
CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG	55
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu	
CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GGC TTC CCC TCC TGC	103
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys	
GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG	151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu	
GCC AAC AGC AGC GGC GGC CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC	199
Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro	
TCT CGA GAC GGC CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG	247
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val	
CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG	295
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu	
TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA	343
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu	
TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC	391
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser	
CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG	439
Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Pro Lys	
TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT	487
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr	

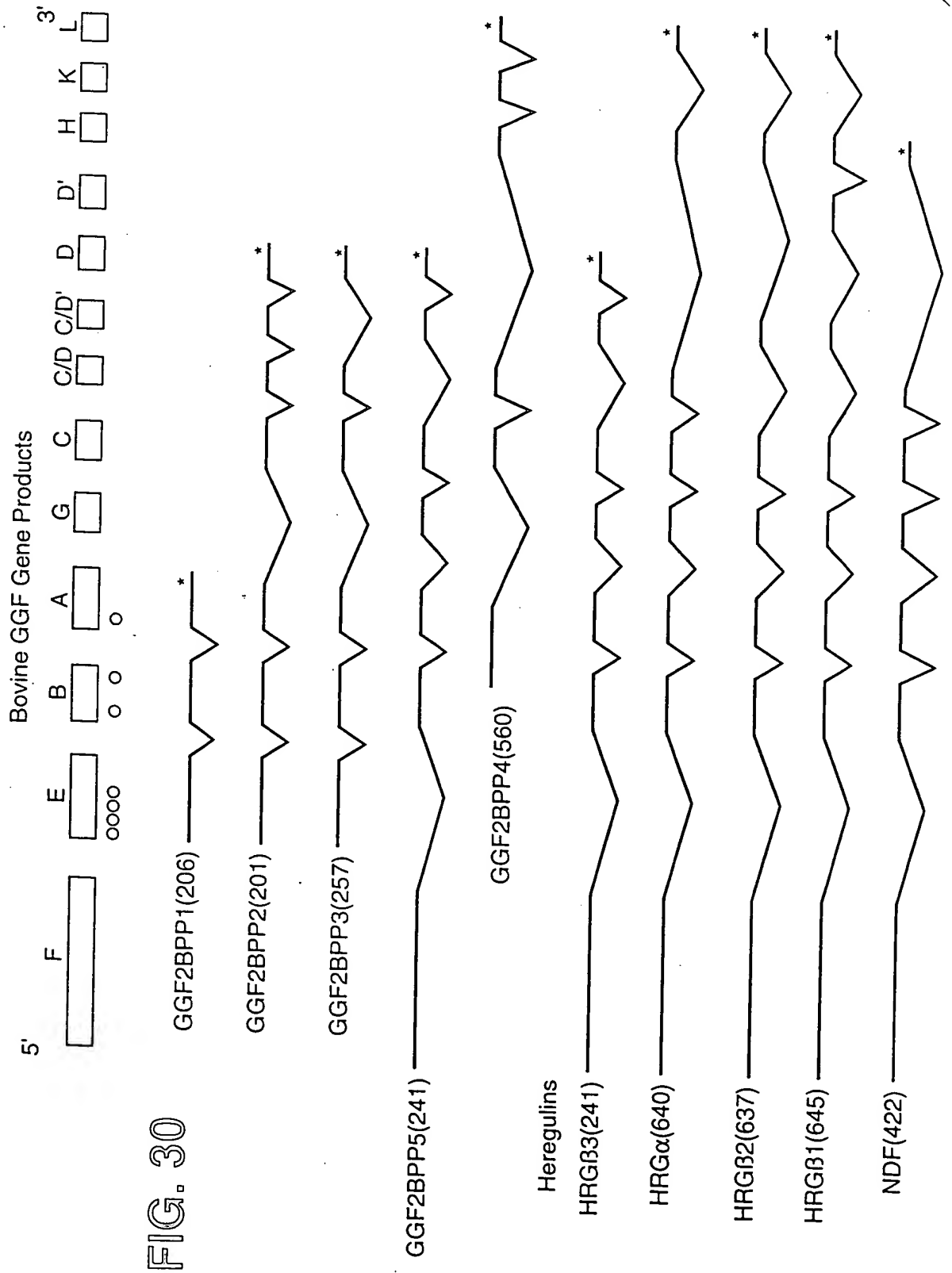
# FIG. 28E

## Nucleotide Sequences & Deduced Amino Acid Sequences of GGF2BPP3

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn	535
ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA Ile Arg Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr	583
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	631
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	679
TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr	727
GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro	775
GAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCGATC TCCCCTCAGA TTCCGCCTAG Glu	838
AGCTAGATGC GTTTTACCAG GTCTAACATT GACTGCCTCT GCCTGTGCGA TGAGAACATT	898
AACACAAGCG ATTGTATGAC TTCTCTCTGTC CGTGACTAGT GGGCTCTGAG CTACTCGTAG	958
GTGCGTAAGG CTCCAGTGTT TCTGAAATTG ATCTTGAATT ACTGTGATAC GACATGATAG	1018
TCCCTCTCAC CCAGTGCAAT GACAATAAAG GCCTTGAAAA GTCAAAAAAAA AAAAAAAA	1078
AAAAATCGAT GTCGACTCGA GATGTGGCTG	1108

FIG. 29





# FIG. 31A

## Coding Segments of Glial Growth Factor/Heregulin Gene

CODING SEGMENT F: (SEQ ID NO: 136 (bovine) and 173 (human))	
AGTTTCCCCC CCAACTTGT CGAACTCTG GGCTCGCGG CAGGGCAGGA GCGAGCGGC	60
GGCGGCTGCC CAGGCGATGC GAGCGCGGGC CGAACGGTAA TCGCCTCTCC CTCCTCGGGC	120
TGCGAGCGCG CCGGACCGAG GCAGCGACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC	180
CCAGCGGCGC GCCAGCAGGA GCCACCCCGC GAGNCGTGCG ACCGGGACGG AGCGCCCGCC	240
AGTCCCAGGT GGCCCGGACC GCACGTTGCG TCCCGCGGCT CCCC CGCGG GACAGGAGAC	300
GCTCCCCCCC ACGCCGCGCG CGCCTCGGCC CGTCTGCTGG CCCGCCCTCCA CTCCGGGGGAC	360
CGCGAG CGCCTCAGCG CGGCGGCTCG CTCTC...CCC CTCGAGGGGAC	
AAACTTTTCC CGAAGCCGAT CCCAGCCCTC GGACCCCAAAC TTGTGCGCGG TCGCCTTCGC	420
AAACTTTTCC CAAACCCGAT CCGAGCCCTT GGACCAA... ..C TCGCCTGCGC	
CGGGAGCCGT CCGCGCAGAG CGTGCACTTC TCGGGCGAG ATG TCG GAG CGC AGA	474
CGAGAGCCGT CCGCGTAGAG CGCTC.CGTC TCCGGCGAG ATG TCC GAG CGC AAA	
Glu Gly Lys Gly Lys Gly Lys Gly Lys Lys Asp Arg Gly Ser Gly	
GAA GGC AAA GGC AAG GGC AAG GGC AAG AAG AAG GAG CGA GGC TCC GGC	522
GAA GGC AGA GGC AAA GGC AAG GGC AAG AAG AAG GAG CGA GGC TCC GGC	
Lys Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala	
AAG AAG CCC GTG CCC GCG GCT GGC GGC CCG AGC CCA G	
AAG AAG CCG GAG TCC GCG GCG GGC AGC CAG AGC CCA G	559

# FIG. 31B

CODING SEGMENT E: (SEQ ID NO: 137)

CC CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser	47
CTG CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser	95
TGC GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Met Glu Pro	143
GAG GCC AAC AGC AGC GGC GGC CCC GGC CGC CTT CCG AGC CTC CTT CCC Glu Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro	191
CCC TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT Pro Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala	239
GTG CAA CGG TGC G Val Gln Arg Cys	252

CODING SEGMENT B: (SEQ ID NO: 138 (bovine, top) and 174 (human, bottom))

Gly	Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	Ser	Ser	Glu	Tyr	Ser	Ser
GGT	TCC	AAA	CTA	GTG	CTT	CGG	TGC	GAG	ACC	AGT	TCT	GAA	TAC	TCC	TCT
GGT	TCC	AAA	CTA	GTC	CTT	CGG	TGT	GAA	ACC	AGT	TCT	GAA	TAC	TCC	TCT

[illegible]

Lys Pro Gln Asn Ile Lys Ile Gln Lys Arg Pro Gly  
AAA CCA CAA AAC ATC AAG ATA CAG AAA AGG CCG GG  
||| ||| ||| ||| ||| ||| ||| ||| |||  
AAA CCA CAA AAT ATC AAG ATA CAA AAA AAG CCA GG

K



Ala Asn Ile Thr Ile Val Glu Ser Asn Ala  
GCC AAC ATC ACC ACC ATT GTG GAG TCA AAC G  
|||| || |||| || |||| || |||| ||||  
GCC AAT ATC ACC ACC ATC GTG GAA TCA AAC G

# FIG. 31E

CODING SEGMENT A': (SEQ ID NO: 140)

TCTAAACTA CAGAGACTGT ATTTTCATGA TCATCATAGT TCTGTGAAAT ATACTTAAAC	60
CGCTTTGGTC CTGATCTTGT AGG AAG TCA GAA CTT CGC ATT AGC AAA GCG	110
Lys Ser Glu Leu Arg Ile Ser Lys Ala	
TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA	158
Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu	
GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC GGT	206
Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Gly	
AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA GGA GTG ATC	254
Lys Arg Cys Leu Leu Arg Ala Ile Ser Gln Ser Leu Arg Gly Val Ile	
AAG GTA TGT GGT CAC ACT TGAATCACGC AGGTGTGTGA AATCTCATTTG	302
Lys Val Cys Gly His Thr	
TGAACAAATA AAAATCATGA AAGGAAAACT CTATGTTTGA AATATCTTAT GGGTCCTCCT	362
GTAAGGCTCT TCACTCCATA AGGTGAAATA GACCTGAAAT ATATATAGAT TATTT	417

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CODING SEGMENT G: (SEQ ID NO: 141 (bovine) and 176 (human))

Glu	Ile	Thr	Thr	Gly	Met	Pro	Ala	Ser	Thr	Glu	Thr	Ala	Tyr	Val	Ser
AG	ATC	ACC	ACT	GGC	ATG	CCA	GCC	TCA	ACT	GAG	ACA	GCG	TAT	GTG	TCT
AG	ATC	ATC	ACT	GGT	ATG	CCA	GCC	TCA	ACT	GAA	GGA	GCA	TAT	GTG	TCT
		I									G				

Ser	Glu	Ser	Pro	Ile	Arg	Ile	Ser	Val	Ser	Thr	Glu	Gly	Thr	Asn	Thr
TCA	GAG	TCT	CCC	ATT	AGA	ATA	TCA	GTA	TCA	ACA	GAA	GGA	ACA	AAT	ACT
													' '		
TCA	GAG	TCT	CCC	ATT	AGA	ATA	TCA	GTA	TCC	ACA	GAA	GGA	GCA	AAT	ACT

Ser Ser Ser  
TCT TCA T  
||| ||| |  
TCT TCA T

CODING SEGMENT C: (SEQ ID NO: 160 (bovine) and 177 (human))

Thr	Ser	Thr	Ser	Thr	Ala	Gly	Thr	Ser	His	Leu	Val	Lys	Cys	Ala	
CC	ACA	TCC	ACA	TCT	ACA	GCT	GGG	ACA	AGC	CAT	CTT	GTC	AAG	TGT	GCA
I															
CT	ACA	TCT	ACA	TCC	ACC	ACT	GGG	ACA	AGC	CAT	CTT	GTA	AAA	TGT	GCG

Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	Gly	Gly	Glu	Cys	Phe	Met	Val
GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT	GGA	GGC	GAG	TGC	TTC	ATG	GTG
GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT	GGA	GGG	GAG	TGC	TTC	ATG	GTG

Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	Leu	Cys
AAA	GAC	CTT	TCA	AAT	CCC	TCA	AGA	TAC	TTG	TGC
AAA	GAC	CTT	TCA	AAC	CCC	TCG	AGA	TAC	TTG	TGC

## 37/78

48

69

Met	Lys	Val	Gln	Thr	Gln	Glu
ATG	AAA	GTC	CAA	ACC	CAA	GAA
ATG	AAA	GTC	CAA	AAC	CAA	GAA
				N		

CODING SEGMENT ~~c/d'~~ (SEQ ID NO: 143 (bovine) and ~~179~~ (human))

48

60

CODING SEGMENT D: (SEQ ID NO: 144 (~~bovine~~) and 180 (~~human~~))

36

CODING SEGMENT D': (SEQ ID NO: 145 (~~bovine~~))

27

## 48

96

144

192

240

288

Ser	Lys	Asn	Val	Ile	Ser	Ser	Glu	His	Ile	Val	Glu	Arg	Glu	Ala	Glu
TCT	AAA	AAT	GTC	ATC	TCT	AGC	GAG	CAT	ATT	GTT	GAG	AGA	GAG	GCG	GAG
TCT	AAA	AAC	GTC	ATC	TCC	AGT	GAG	CAT	ATT	GTT	GAG	AGA	GAA	GCA	GAG

# FIG. 31M

Ser	Ser	Phe	Ser	Thr	Ser	His	Tyr	Thr	Ser	Thr	Ala	His	His	Ser	Thr		336
AGC	TCT	TTT	TCC	ACC	AGT	CAC	TAC	ACT	TCG	ACA	GCT	CAT	CAT	TCC	ACT		
ACA	TCC	TTT	TCC	ACC	AGT	CAC	TAT	ACT	TCC	ACA	GCC	CAT	CAC	TCC	ACT		
T																	
Thr	Val	Thr	Gln	Thr	Pro	Ser	His	Ser	Trp	Ser	Asn	Gly	His	Thr	Glu		384
ACT	GTC	ACT	CAG	ACT	CCC	AGT	CAC	AGC	TGG	AGC	AAT	GGA	CAC	ACT	GAA		
ACT	GTC	ACC	CAG	ACT	CCT	AGC	CAC	AGC	TGG	AGC	AAC	GGA	CAC	ACT	GAA		
Ser	Ile	Ile	Ser	Glu	Ser	His	Ser	Val	Ile	Val	Met	Ser	Ser	Val	Glu		432
AGC	ATC	ATT	TCG	GAA	AGC	CAC	TCT	GTC	ATC	GTG	ATG	TCA	TCC	GTA	GAA		
AGC	ATC	CTT	TCC	GAA	AGC	CAC	TCT	GTA	ATC	GTG	ATG	TCA	TCC	GTA	GAA		
L																	
Asn	Ser	Arg	His	Ser	Ser	Pro	Thr	Gly	Gly	Pro	Arg	Gly	Arg	Leu	Asn		480
AAC	AGT	AGG	CAC	AGC	AGC	CCG	ACT	GGG	GGC	CCG	AGA	GGA	CGT	CTC	AAT		
AAC	AGT	AGG	CAC	AGC	AGC	CCA	ACT	GGG	GGC	CCA	AGA	GGA	CGT	CTT	AAT		
Gly	Leu	Gly	Gly	Pro	Arg	Glu	Cys	Asn	Ser	Phe	Leu	Arg	His	Ala	Arg		528
GGC	TTG	GGA	GGC	CCT	CGT	GAA	TGT	AAC	AGC	TTC	CTC	AGG	CAT	GCC	AGA		
GGC	ACA	GGA	GGC	CCT	CGT	GAA	TGT	AAC	AGC	TTC	CTC	AGG	CAT	GCC	AGA		
T																	
Glu	Thr	Pro	Asp	Ser	Tyr	Arg	Asp	Ser	Pro	His	Ser	Glu	Arg				569
GAA	ACC	CCT	GAC	TCC	TAC	CGA	GAC	TCT	CCT	CAT	AGT	GAA	AG				
GAA	ACC	CCT	GAT	TCC	TAC	CGA	GAC	TCT	CCT	CAT	AGT	GAA	AG				



# FIG. 31N

CODING SEGMENT K: (SEQ ID NO: 161)

A	CAT	AAC	CTT	ATA	GCT	GAG	CTA	AGG	AGA	AAC	AAG	GCC	CAC	AGA	TCC	46
	His	Asn	Leu	Ile	Ala	Glu	Leu	Arg	Arg	Asn	Lys	Ala	His	Arg	Ser	
AAA	TGC	ATG	CAG	ATC	CAG	CTT	TCC	GCA	ACT	CAT	CTT	AGA	GCT	TCT	TCC	94
	Lys	Cys	Met	Gln	Ile	Gln	Leu	Ser	Ala	Thr	His	Leu	Arg	Ala	Ser	
ATT	CCC	CAT	TGG	GCT	TCA	TTC	TCT	AAG	ACC	CCT	TGG	CCT	TTA	GGA	AG	141
	Ile	Pro	His	Trp	Ala	Ser	Phe	Ser	Lys	Thr	Pro	Trp	Pro	Leu	Gly	Arg

# FIG. 310

CODING SEGMENT L: (SEQ ID NO: 147 (bovine) and 182 (human))

Tyr Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro Val Asp	46
G TAT GTA TCA GCA ATG ACC ACC CCG GCT CGT ATG TCA CCT GTA GAT	
G TAT GTG TCA GCC ATG ACC ACC CCG GCT CGT ATG TCA CCT GTA GAT	
Phe His Thr Pro Ser Ser Thr Thr Val Ser Met Pro Ser Glu Met Ser Pro	94
TTC CAC ACG CCA AGC TCC CCC AAG TCA CCC CCT TCG GAA ATG TCC CCG	
TTC CAC ACG CCA AGC TCC CCC AAA TCG CCC CCT TCG GAA ATG TCT CCA	
Pro Val Ser Ser Thr Thr Thr Val Ser Met Pro Ser Met Ala Val Ser Pro	142
CCC GTG TCC AGC ACG ACG GTC TCC ATG CCC TCC ATG GCG GTC AGT CCC	
CCC GTG TCC AGC ATG ACG GTG TCC ATG CCC TCC ATG GCG GTC AGC CCC	
Phe Val Glu Glu Glu Arg Pro Leu Leu Leu Val Thr Pro Pro Arg Leu	190
TTC GTG GAA GAG GAG AGA CCC CTG CTC CTT GTG ACG CCA CCA CGG CTG	
TTC ATG GAA GAA GAG AGA CCT CTA CTT CTC GTG ACA CCA CCA AGG CTG	
Arg Glu Lys - Tyr Asp His His Ala Gln Gln Phe Asn Ser Phe His	238
CGG GAG AAG ... TAT GAC CAC CAC GCC CAG CAA TTC AAC TCG TTC CAC	
CGG GAG AAG AAG TTT GAC CAT CAC CCT CAG CAG TTC AGC TCC TTC CAC	
Cys Asn Pro Ala His Glu Ser Asn Ser Leu Pro Pro Ser Pro Leu Arg	286
TGC AAC CCC GCG CAT GAG AGC AAC AGC AGC CTG CCC CCC AGC CCC TTG AGG	
CAC AAC CCC GCG CAT GAC AGT AAC AGC AGC CTC CCT GCT AGC CCC TTG AGG	

**FIG. 31P**

[illegible]

# FIG. 31Q

Val Gly Glu Asp Thr Pro Phe Leu Ala Ile Gln Asn Pro Leu Ala Ala	526
GTA GGA GAA GAT ACG CCT TTC CTG GCC ATA CAG AAC CCC CTG GCA GCC	
GTA GGT GAA GAT ACG CCT TTC CTG GGC ATA CAG AAC CCC CTG GCA GCC	
G	
Ser Leu Glu Ala Ala Pro Ala Phe Arg Leu Val Asp Ser Arg Thr Asn	574
AGT CTC GAG GCG GCC CCT CCT GGC CTG GTC GAC AGC AGG ACT AAC	
AGT CTT GAG GCA ACA CCT GGC TTC CGC CTG GCT GAC AGC AGG ACT AAC	
A	
Pro Thr Gly Gly Phe Ser Pro Gln Glu Leu Gln Ala Arg Leu Ser	622
CCA ACA GGC GGC TTC TCT CCG CAG GAA GAA TTG CAG GCC AGG CTC TCC	
CCA GCA GGC CGC TTC TCG ACA CAG GAA GAA ATC CAG GCC AGG CTG TCT	
A R	
Gly Val Ile Ala Asn Gln Asp Pro Ile Ala Val *	672
GGT GTA ATC GCT AAC CAA GAC CCT ATC GCT GTC TAA AAC CGA AAT ACA	
AGT GTA ATT GCT AAC CAA GAC CCT ATT GCT GTA TAA AAC CTA AAT AAA	
S	
CCC ATA GAT TCA CCT GTA AAA CTT TAT TTT ATA TAA TAA AGT ATT CCA	718
CAC ATA GAT TCA CCT GTA AAA CTT TAT TTT ATA TAA TAA AGT ATT CCA	
CCT TAA ATT AAA CAA	733
CCT TAA ATT AAA CAA	

# FIG. 31R

HUMAN CODING SEGMENT E:  
(SEQ ID NO: 163)

ATG AGA TGG CGA CGC GCC CGC CGC TCC GGG CGT CCC GGC CCC CGG	48
Met Arg Trp Arg Arg Ala Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg	
GCC CAG CGC CCC GGC TCC GCC GCC CGC TCG CCG CCG CTG CCG CTG	96
Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu	
CTG CCA CTA CTG CTG CTG GGG ACC GCG GCC CTG GCG CCG GGG GCG	144
Leu Pro Leu Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala	
GCG GCC GGC AAC GAG GCG GCT CCC GCG GGG GCC TCG GTG TGC TAC TCG	192
Ala Ala Gly Asn Glu Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser	
TCC CCG CCC AGC GTG GGA TCG GTG CAG GAG CTA GCT CAG CGC GCC GCG	240
Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala	
GTG GTG ATC GAG GGA AAG GTG CAC CCG CAG CGG CAG CAG GGG GCA	288
Val Val Ile Glu Gly Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala	
CTC GAC AGG AAG GCG GCG GCG GCG GGC GAG GCA GGG GCG TGG GGC	336
Leu Asp Arg Lys Ala Ala Ala Ala Gly Glu Ala Gly Ala Trp Gly	
GGC GAT CGC GAG CCG CCA GCC GCG GGC CCA CCG CTG GGG CCG CCC	384
Gly Asp Arg Glu Pro Pro Ala Ala Gly Pro Arg Ala Leu Gly Pro Pro	
GCC GAG GAG CCG CTG CTC GCC GCC AAC GCG ACC GTG CCC TCT TGG CCC	432
Ala Glu Glu Pro Leu Leu Ala Ala Asn Gly Thr Val Pro Ser Trp Pro	
ACC GCC CCG GTG CCC AGC GCC GGC GAG CCC GGG GAG GAG GCG CCC TAT	480
Thr Ala Pro Val Pro Ser Ala Gly Glu Pro Gly Glu Glu Ala Pro Tyr	
CTG GTG AAG GTG CAC CAG GTG TGG GCG GTG AAA GCC GGG GGC TTG AAG	528
Leu Val Lys Val His Gln Val Trp Ala Val Lys Ala Gly Gly Leu Lys	
AAG GAC TCG CTG CTC ACC GTG CGC CTG GGG ACC TGG GCG CAC CCC GCC	576
Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Thr Trp Gly His Pro Ala	
TTC CCC TCC TGC GGG AGG CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC	624
Phe Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe	
ATG GAG CCC GAC GCC AAC AGC ACC AGC CGC GCG CCG GCC TTC CGA	672
Met Glu Pro Asp Ala Asn Ser Thr Ser Arg Ala Pro Ala Phe Arg	
GCC TCT TTC CCC CCT CTG GAG ACG GCG AAC CTC AAG AAG GAG GTC	720
Ala Ser Phe Pro Pro Leu Glu Thr Gly Arg Asn Leu Lys Glu Val	
AGC CCG GTG CTG TGC AAG CCG TGC G	745
Ser Arg Val Leu Cys Lys Arg Cys	

# **FIG. 32A** **GGF2BPP5 Nucleotide Sequence & Deduced Protein Sequence**

SEQ ID NO: 148:		
AGTTTCCCCC	CCAAACTTGT CGGAACCTCTG GGCTCGCGCG CAGGGCAGGA GCGGAGCGGC	60
GGCGGCTGCC	CAGGCGATGC GAGCGCGGGC CGGACGGTAA TCGCCTCTCC CTCCTCGGGC	120
TGCGAGCGCG	CCGGACCGAG GCAGCGACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC	180
CCAGCGGCGC	GCCAGCAGGA GCCACCCCGC GAGCGTGCGA CCGGGACGGA GCGCCCGCCA	240
GTCCAGGTG	GCCCGGACCG CACGTTGCGT CCCC CGCGCTC CCCGCCGCG ACAGGAGACG	300
CTCCCCCCCC	CGCCGCGCGC GCCTCGGCCC GGTCGCTGGC CCGCCTCCAC TCCGGGGACA	360
AACTTTTCCC	GAAGCCGATC CCAGCCCTCG GACCCAAACT TGTCGCGCGT CGCCTTCGCC	420
GGGAGCCGTC	CGCGCAGAGC GTGCACTTCT CGGGCGAG ATG TCG GAG CGC AGA	475
	Met Ser Glu Arg Arg	
GAA GGC AAA	GGC AAG GGG AAG GGC GGC AAG AAG GAC CGA GGC TCC GGG	523
Glu Gly Lys	Gly Lys Lys Gly Lys Lys Lys Asp Arg Gly Ser Gly	
AAG AAG CCC	GTG CCC GCG GCT GGC GGC CCG AGC CCA GCC TTG CCT CCC	571
Lys Lys Pro	Val Pro Ala Ala Gly Gly Pro Ser Pro Ala Leu Pro Pro	
CGC TTG AAA	GAG ATG AAG ATG CAG GAG TCT GTG GCA GGT TCC AAA CTA	619
Arg Leu Lys	Glu Met Lys Ser Gln Glu Ser Val Ala Gly Ser Lys Leu	
GTG CTT CGG	TGC GAG ACC AGT TCT GAA TAC TCC TCT CTC AAG TTC AAG	667
Val Leu Arg	Cys Glu Thr Ser Ser Ser Glu Tyr Ser Ser Leu Lys Phe Lys	
TGG TTC AAG	AAT GGG AGT GAA TTA AGC CGA AAG AAC AAA CCA CAA AAC	715
Trp Phe Lys	Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys Pro Gln Asn	
ATC AAG ATA	CAG AAA AGG CCG GGG AAG TCA GAA CTT CGC ATT AGC AAA	763
Ile Lys Ile	Gln Lys Arg Pro Gly Lys Ser Glu Leu Arg Ile Ser Lys	
GCG TCA CTG	GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA	811
Ala Ser Leu	Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys	

# FIG. 32B

## GGF2BPP5 Nucleotide Sequence & Deduced Protein Sequence

CTA GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn	859
GAG ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT Glu Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser	907
TCA GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr	955
TCT TCA TCC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG Ser Ser Ser Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys	1003
TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe	1051
ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC TTG TGC AAG TGC CCA Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro	1099
AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe	1147
TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAGGCGCATG Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu	1193
CTCAGTCGGT GCCGCTTTCT TGTGCCGCA TCTCCCCCTCA GATTCAACCT AGAGCTAGAT	1253
GCGTTTACC AGGTCTAACA TTGACTGCCT CTGCCCTGTCG CATGAGAACA TTAACACAAG	1313
CGATTGTATG ACTTCCTCTG TCCGTGACTA GTGGGCTCTG AGCTACTCGT AGGTGCGTAA	1373
GGCTCCAGTG TTTCTGAAAT TGATCTTGAA TTA CTGTGTAT ACGACATGAT AGTCCCCTCTC	1433
ACCCAGTGCA ATGACAATAA AGGCCTTGAA AAGTCTCACT TTTATTGAGA AAATAAAAAAT	1493
CGTTCCACGG GACAGTCCCT CTTCTTTTATA AAATGACCCT ATCCTTGAAA AGGAGGTGTG	1553
TTAAGTTGTA ACCAGTACAC ACTTGAAATG ATGTAAGTT CGCTTCGGTT CAGAATGTGT	1613
TCTTTCTGAC AAATAAACAG AATAAAAAA AAAAAAAAA A	1654

# **FIG. 33A** **GGF2BPP2 Nucleotide Sequence & Deduced Protein Sequence**

SEQ ID NO: 149:

CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG	48
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu	
CTC ACC GTG CGC CTG GGC GGC GGC TGG GGC CAC CCC GCC TTC CCC TCC TGC	96
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys	
GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG	144
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Met Glu Pro Glu	
GCC AAC AGC AGC GGC GGC CCC GGC CTT CCG AGC CTC CTT CCC CCC	192
Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro	
TCT CGA GAC GGC CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG	240
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val	
CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG	288
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu	
TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA	336
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu	
TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC	384
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser	
CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG	432
Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys	
TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT	480
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr	
ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC	528
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn	



# **FIG. 33B** **GGF2BPP2 Nucleotide Sequence & Deduced Protein Sequence**

ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr	576
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	624
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	672
TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn	720
GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr	768
GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser	816
ACT CCC TTT CTG TCT CTG CCT GAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG Thr Pro Phe Leu Ser Leu Pro Glu	870
TTGCCGCATC TCCCCCTCAGA TTCCNCCTAG AGCTAGATGC GTTTTACCAG GTCTAACATT	930
GACTGCCTCT GCCTGTCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCTCTGTC	990
CGTGACTAGT GGGCTCTGAG CTA CTCTCGTAG GTGCGTAAGG CTCCAGTGT TCTGAAATTG	1050
ATCTTGAATT ACTGTGATAC GACATGATAG TCCCTCTCAC CCAGTGCAAT GACAATAAAG	1110
GCCTTGAAAA GTCAAAAAAA AAAAAAAAAA	1140

# **FIG. 34A** **GGF2BPP4 Nucleotide Sequence & Deduced Protein Sequence**

SEQ ID NO: 150:

G AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu	49
TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala	97
AAC ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG Asn Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly	145
ACA AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val	193
AAT GGA GGC GAC TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA Asn Gly Gly Asp Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg	241
TAC TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu	289
AAT GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC Asn Val Pro Met Lys Val Lys Val Gln Thr Gln Glu Lys Ala Glu Leu Tyr	337
CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT TGC ATC GCG CTG CTC GTG Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val	385
GTT GGC ATC ATG TGT GTG GTC TAC TGC AAA ACC AAG AAA CAA CCG Val Gly Ile Met Cys Val Val Tyr Cys Lys Thr Lys Lys Gln Arg	433
AAA AAG CTT CAT GAC CCG CTT CCG CAG AGC CTT CGG TCT GAA AGA AAC Lys Lys Leu His Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn	481
ACC ATG ATG AAC GTA GCC AAC GGG CCC CAC CAC CCC AAT CCG CCC CCC Thr Met Met Asn Val Ala Asn Gly Pro His His Pro Asn Pro Pro Pro	529
GAG AAC GTG CAG CTG GTG AAT CAA TAC GTA TCT AAA AAT GTC ATC TCT Glu Asn Val Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser	577

# **FIG. 34B** **GGF2BPP4 Nucleotide Sequence & Deduced Protein Sequence**

AGC GAG CAT ATT GTT GAG AGA GAG GCG GAG AGC TCT TTT TCC ACC AGT Ser Glu His Ile Val Glu Arg Glu Ala Glu Ser Ser Phe Ser Thr Ser	625
CAC TAC ACT TCG ACA GCT CAT CAT TCC ACT ACT GTC ACT CAG ACT CCC His Tyr Thr Ser Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro	673
AGT CAC AGC TGG AGC AAT GGA CAC ACT GAA AGC ATC ATT TCG GAA AGC Ser His Ser Trp Ser Ser Asn Gly His Thr Glu Ser Ile Ser Glu Ser	721
CAC TCT GTC ATC GTG ATG TCA TCC GTA GAA AAC AGT AGG CAC AGC AGC His Ser Val Ile Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser	769
CCG ACT GGG GGC CCG AGA GGA CGT CTC AAT GGC TTG GGA GGC CCT CGT Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn Gly Leu Gly Gly Pro Arg	817
GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA GAA ACC CCT GAC TCC TAC Glu Cys Asn Ser Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr	865
CGA GAC TCT CCT CAT AGT GAA AGA CAT AAC CTT ATA GCT GAG CTA AGG Arg Asp Ser Pro His Ser Glu Arg His Asn Leu Ile Ala Glu Leu Arg	913
AGA AAC AAG GCC CAC AGA TCC AAA TGC ATG CAG ATC CAG CTT TCC GCA Arg Asn Lys Ala His Arg Ser Lys Cys Met Gln Ile Gln Leu Ser Ala	961
ACT CAT CTT AGA GCT TCT TCC ATT CCC CAT TGG GCT TCA TTC TCT AAG Thr His Leu Arg Ala Ser Ser Ile Pro His Trp Ala Ser Phe Ser Lys	1009
ACC CCT TGG CCT TTA GGA AGG TAT GTA TCA GCA ATG ACC ACC CCG GCT Thr Pro Trp Pro Leu Gly Arg Tyr Val Ser Ala Met Thr Thr Pro Ala	1057
CGT ATG TCA CCT GTA GAT TTC CAC ACG CCA AGC TCC CCC AAG TCA CCC Arg Met Ser Pro Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro	1105
CCT TCG GAA ATG TCC CCG CCC GTG TCC AGC ACG GTC TCC ATG CCC Pro Ser Glu Met Ser Pro Pro Val Ser Ser Thr Thr Val Ser Met Pro	1153

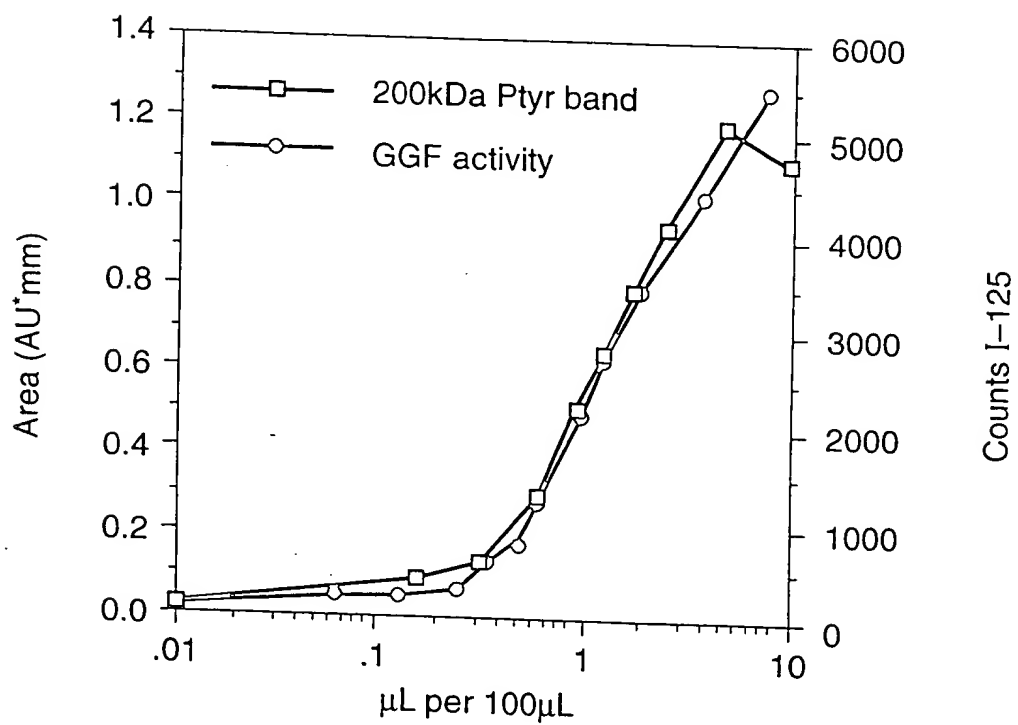
# FIG. 34C

## GGF2BPP4 Nucleotide Sequence & Deduced Protein Sequence

TCC ATG GCG GTC AGT CCC TTC GTG GAA GAG GAG AGA CCC CTG CTC CTT Ser Met Ala Val Ser Pro Phe Val Glu Glu Arg Pro Leu Leu Leu	1201
GTG ACG CCA CCA CCG CTG CCG GAG AAG TAT GAC CAC CAC GCC CAG CAA Val Thr Pro Pro Arg Leu Arg Glu Lys Tyr Asp His Ala Gln Gln	1249
TTC AAC TCG TTC CAC TGC AAC CCC GCG CAT GAG AGC AAC AGC CTG CCC Phe Asn Ser Phe His Cys Asn Pro Ala His Glu Ser Asn Ser Leu Pro	1297
CCC AGC CCC TTG AGG ATA GTG GAG GAT GAG GAA TAT GAA ACG ACC CAG Pro Ser Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln	1345
GAG TAC GAA CCA GCT CAA GAG CCG GTT AAG AAA CTC ACC AAC AGC AGC Glu Tyr Glu Pro Ala Gln Glu Pro Val Lys Lys Leu Thr Asn Ser Ser	1393
CGG CGG GCC AAA AGA ACC AAG CCC AAT GGT CAC ATT GCC CAC AGG TTG Arg Arg Ala Lys Arg Thr Lys Pro Asn Gly His Ile Ala His Arg Leu	1441
GAA ATG GAC AAC AAC ACA GGC GCT GAC AGC AGT AAC TCA GAG AGC GAA Glu Met Asp Asn Asn Thr Gly Ala Asp Ser Ser Asn Ser Glu Ser Glu	1489
ACA GAG GAT GAA AGA GTA GGA GAA GAT ACG CCT TTC CTG GCC ATA CAG Thr Glu Asp Glu Arg Val Gly Glu Asp Thr Pro Phe Leu Ala Ile Gln	1537
AAC CCC CTG GCA GCC AGT CTC GAG GCG GCC CCT GCC TTC CGC CTG GTC Asn Pro Leu Ala Ala Ser Leu Glu Ala Ala Pro Ala Phe Arg Leu Val	1585
GAC AGC AGG ACT AAC CCA ACA GGC GGC TTC TCT CCG CAG GAA GAA TTG Asp Ser Arg Thr Asn Pro Thr Gly Gly Phe Ser Pro Gln Glu Glu Leu	1633
CAG GCC AGG CTC TCC GGT GTA ATC GCT AAC CAA GAC CCT ATC GCT GTC Gln Ala Arg Leu Ser Gly Val Ile Ala Asn Gln Asp Pro Ile Ala Val	1681
TAAAACCGAA ATACACCCCAT AGATTACCT GTAAACCTTT ATTTTATATA ATAAAGTATT CCACCTTAAA TTAACACAAA AAA	1741 1764

## hEGF

**FIG. 36**  
**200 kDa Tyrosine Phosphorylation**  
**Compared with Mitogenic Activity**



# FIG. 37A GGF/Heregulin Splicing Variants

F-B-A'

F-B-A-C-C/D-D  
 F-B-A-C-C/D-H  
 F-B-A-C-C/D-H-L  
 F-B-A-C-C/D-H-K-L  
 F-B-A-C-C/D-D'-H  
 F-B-A-C-C/D-D'-H-L  
 F-B-A-C-C/D-D'-H-K-L  
 F-B-A-C-C/D'-D  
 F-B-A-C-C/D'-H  
 F-B-A-C-C/D'-H-L  
 F-B-A-C-C/D'-H-K-L  
 F-B-A-C-C/D'-D'-H  
 F-B-A-C-C/D'-D'-H-L  
 F-B-A-C-C/D'-D'-H-K-L  
 F-B-A-C-C/D-C/D'-D  
 F-B-A-C-C/D-C/D'-H  
 F-B-A-C-C/D-C/D'-H-L  
 F-B-A-C-C/D-C/D'-H-K-L  
 F-B-A-C-C/D-C/D'-D'-H  
 F-B-A-C-C/D-C/D'-D'-H-L  
 F-B-A-C-C/D-C/D'-D'-H-K-L

F-B-A-G-C-C/D-D  
 F-B-A-G-C-C/D-H  
 F-B-A-G-C-C/D-H-L  
 F-B-A-G-C-C/D-H-K-L  
 F-B-A-G-C-C/D-D'-H  
 F-B-A-G-C-C/D-D'-H-L  
 F-B-A-G-C-C/D-D'-H-K-L  
 F-B-A-G-C-C/D'-D  
 F-B-A-G-C-C/D'-H  
 F-B-A-G-C-C/D'-H-L  
 F-B-A-G-C-C/D'-H-K-L  
 F-B-A-G-C-C/D'-D'-H  
 F-B-A-G-C-C/D'-D'-H-L  
 F-B-A-G-C-C/D'-D'-H-K-L  
 F-B-A-G-C-C/D-C/D'-D  
 F-B-A-G-C-C/D-C/D'-H  
 F-B-A-G-C-C/D-C/D'-H-L  
 F-B-A-G-C-C/D-C/D'-H-K-L  
 F-B-A-G-C-C/D-C/D'-D'-H  
 F-B-A-G-C-C/D-C/D'-D'-H-L  
 F-B-A-G-C-C/D-C/D'-D'-H-K-L

F-E-B-A'

F-E-B-A-C-C/D-D  
 F-E-B-A-C-C/D-H  
 F-E-B-A-C-C/D-H-L  
 F-E-B-A-C-C/D-H-K-L  
 F-E-B-A-C-C/D-D'-H  
 F-E-B-A-C-C/D-D'-H-L  
 F-E-B-A-C-C/D-D'-H-K-L  
 F-E-B-A-C-C/D'-D  
 F-E-B-A-C-C/D'-H  
 F-E-B-A-C-C/D'-H-L  
 F-E-B-A-C-C/D'-H-K-L  
 F-E-B-A-C-C/D'-D'-H  
 F-E-B-A-C-C/D'-D'-H-L  
 F-E-B-A-C-C/D'-D'-H-K-L  
 F-E-B-A-C-C/D-C/D'-D  
 F-E-B-A-C-C/D-C/D'-H  
 F-E-B-A-C-C/D-C/D'-H-L  
 F-E-B-A-C-C/D-C/D'-H-K-L  
 F-E-B-A-C-C/D-C/D'-D'-H  
 F-E-B-A-C-C/D-C/D'-D'-H-L  
 F-E-B-A-C-C/D-C/D'-D'-H-K-L

F-E-B-A-G-C-C/D-D  
 F-E-B-A-G-C-C/D-H  
 F-E-B-A-G-C-C/D-H-L  
 F-E-B-A-G-C-C/D-H-K-L  
 F-E-B-A-G-C-C/D-D'-H  
 F-E-B-A-G-C-C/D-D'-H-L  
 F-E-B-A-G-C-C/D-D'-H-K-L  
 F-E-B-A-G-C-C/D'-D  
 F-E-B-A-G-C-C/D'-H  
 F-E-B-A-G-C-C/D'-H-L  
 F-E-B-A-G-C-C/D'-H-K-L  
 F-E-B-A-G-C-C/D'-D'-H  
 F-E-B-A-G-C-C/D'-D'-H-L  
 F-E-B-A-G-C-C/D'-D'-H-K-L  
 F-E-B-A-G-C-C/D-C/D'-D  
 F-E-B-A-G-C-C/D-C/D'-H  
 F-E-B-A-G-C-C/D-C/D'-H-L  
 F-E-B-A-G-C-C/D-C/D'-H-K-L  
 F-E-B-A-G-C-C/D-C/D'-D'-H  
 F-E-B-A-G-C-C/D-C/D'-D'-H-L  
 F-E-B-A-G-C-C/D-C/D'-D'-H-K-L

# FIG. 37B

GGF/Heregulin  
Splicing Variants

E-B-A'

E-B-A-C-C/D-D  
 E-B-A-C-C/D-H  
 E-B-A-C-C/D-H-L  
 E-B-A-C-C/D-H-K-L  
 E-B-A-C-C/D-D'-H  
 E-B-A-C-C/D-D'-H-L  
 E-B-A-C-C/D-D'-H-K-L  
 E-B-A-C-C/D'-D  
 E-B-A-C-C/D'-H  
 E-B-A-C-C/D'-H-L  
 E-B-A-C-C/D'-H-K-L  
 E-B-A-C-C/D'-D'-H  
 E-B-A-C-C/D'-D'-H-L  
 E-B-A-C-C/D'-D'-H-K-L  
 E-B-A-C-C/D-C/D'-D  
 E-B-A-C-C/D-C/D'-H  
 E-B-A-C-C/D-C/D'-H-L  
 E-B-A-C-C/D-C/D'-H-K-L  
 E-B-A-C-C/D-C/D'-D'-H  
 E-B-A-C-C/D-C/D'-D'-H-L  
 E-B-A-C-C/D-C/D'-D'-H-K-L

E-B-A-G-C-C/D-D  
 E-B-A-G-C-C/D-H  
 E-B-A-G-C-C/D-H-L  
 E-B-A-G-C-C/D-H-K-L  
 E-B-A-G-C-C/D-D'-H  
 E-B-A-G-C-C/D-D'-H-L  
 E-B-A-G-C-C/D-D'-H-K-L  
 E-B-A-G-C-C/D'-D  
 E-B-A-G-C-C/D'-H  
 E-B-A-G-C-C/D'-H-L  
 E-B-A-G-C-C/D'-H-K-L  
 E-B-A-G-C-C/D'-D'-H  
 E-B-A-G-C-C/D'-D'-H-L  
 E-B-A-G-C-C/D'-D'-H-K-L  
 E-B-A-G-C-C/D-C/D'-D  
 E-B-A-G-C-C/D-C/D'-H  
 E-B-A-G-C-C/D-C/D'-H-L  
 E-B-A-G-C-C/D-C/D'-H-K-L  
 E-B-A-G-C-C/D-C/D'-D'-H  
 E-B-A-G-C-C/D-C/D'-D'-H-L  
 E-B-A-G-C-C/D-C/D'-D'-H-K-L



# **FIG. 38** **EGFL1**

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SEQ ID NO: 154:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT	48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	
GGA GGC GAG TGC TTC ATG ATG GAC CTT TCA AAT CCC TCA AGA TAC	96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	
TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC	144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr	
GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT	192
Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro	
GAA TAG	198
Glu	

# **FIG. 39** EGFL2

SEQ ID NO: 155:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT	48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	
GGA GGC GAG TGC TTC ATG ATG GAC CTT TCA AAT CCC TCA AGA TAC	96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	
TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT	144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn	
GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC TAA	192
Val Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Glu Leu Tyr	

# FIG. 40

EGFL3

SEQ ID NO: 156:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48  
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96  
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC 144  
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr

GTA ATG GCC AGC TTC TAC AAA GCG GAG GAG CTC TAC TAA 183  
Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu Tyr

# FIG. 41

## EGFL4

SEQ ID NO: 157:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT	48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC	96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	
TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC	144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr	
GTA ATG GCC AGC TTC TAC AAG CAT CTT GGG ATT GAA TTT ATG GAG AAA	192
Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu Phe Met Glu Lys	
GCG GAG GAG CTC TAC TAA	210
Ala Glu Glu Leu Tyr	

# FIG. 42 EGFL5

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SEQ ID NO: 158:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT	48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC	96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	
TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT	144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn	
GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT	192
Val Pro Met Lys Val Lys Thr Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr	
GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC	240
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser	
ACT CCC TTT CTG TCT CTG CCT GAA TAG	267
Thr Pro Phe Leu Ser Leu Pro Glu	

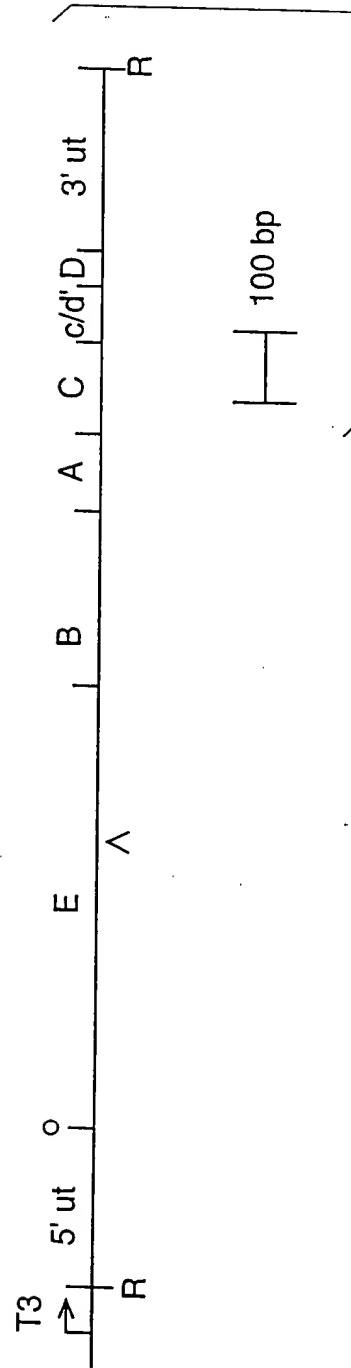
# FIG. 43 EGFL6

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SEQ ID NO: 159:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT	48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC	96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	
TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT	144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn	
GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TCC CCA AAT GAG TTT ACT	192
Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr	
GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AAA GCG GAG	240
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys Ala Glu	
GAG CTC TAC TAA	252
Glu Leu Tyr	

**FIG. 44**  
GGF2HBS5



# **FIG. 45A** **Nucleotide Sequence & Deduced Acid Sequence of GGF2HBS5**

SEQ ID NO: 21:

GGAATTCCTT	TTTTTTTTTT	TTTTTTTTTT	NNTTTTTTT	TGCCCTTATA	CCTCTTCGCC	60
TTTCTGTGGT	TCCATCCACT	TCTTCCCCCT	CCTCCTCCCA	TAAACAACATC	TCCTACCCCT	120
GCACCCCCAA	TAAATAAATA	AAAGGAGGAG	GGCAAGGGGG	GAGGAGGAGG	AGTGGTGCTG	180
CGAGGGGAAG	GAAAAGGGAG	GCAGCGCGAG	AAGAGCCGGG	CAGAGTCCGA	ACCGACAGCC	240
AGAAGCCCGC	ACGCACCTCG	CACC	ATG AGA TGG CGA CGC GCC CCG CGC CGC			291
			Met Arg Trp Arg Arg Ala Pro Arg Arg			
TCC GGG CGT CCC GGC CCC GCG GCC CAG CGC CCC GGC TCC GCC GCC CGC						339
Ser Gly Arg Pro Gly Pro Arg Ala Gln Arg Pro Gly Ser Ala Ala Arg						
TCG TCG CCG CCG CTG CCG CTG CCA CTA CTG CTG CTG CTG GGG ACC						387
Ser Ser Pro Pro Leu Pro Leu Leu Pro Leu Leu Leu Leu Thr Val						
			Val Cys Leu Leu Thr Val			
			GGF-II 09			
GCG GCC CTG CCG CCG GCG GCG GCG GCC AAC GAG GCG GCT CCC GCG						435
Ala Ala Leu Ala Pro Gly Ala Ala Ala Gly Asn Glu Ala Ala Pro Ala						
Ala Ala Leu Pro Pro						
GGG GCC TCG GTG TGC TAC TCG TCC CCG CCC AGC GTG GGA TCG GTG CAG						483
Gly Ala Ser Val Cys Tyr						
			Ala Ser Pro Val Ser Val Gly Ser Val Gln			
			GGF-II 08			
GAG CTA GCT CAG CGC GCC GCG GTG ATC GAG GGA AAG GTG CAC CCG						531
Glu Leu Ala Gln Arg Ala Ala Val Val Ile Glu Gly Lys Val His Pro						
Glu Leu Val Gln Arg Trp Phe Val Val Ile Glu Gly Lys						
			GGF-II 04			



# FIG. 45B

## Nucleotide Sequence & Deduced Acid Sequence of GGF2HBS5

CAG CGG CGG CAG CAG GGG GCA CTC GAC AGG AAG GCG GCG GCG GCG GCG	579
Gln Arg Arg Gln Gln Gly Ala Leu Asp Arg Lys Ala Ala Ala Ala	
GGC GAG GCA GGG GCG TGG GGC GGC GAT CGC GAG CCG CCA GCC GCG GGC	627
Gly Glu Ala Gly Ala Trp Gly Gly Asp Arg Glu Pro Pro Ala Ala Gly	
CCA CGG GCG CTG GGG CCG CCC GCG GAG GAG CCG CTG CTC GCC GCC AAC	675
Pro Arg Ala Leu Gly Pro Pro Ala Glu Glu Pro Leu Leu Ala Ala Asn	
GGG ACC GTG CCC TCT TGG CCC ACC GCC CCG GTG CCC AGC GCC GGC GAG	723
Gly Thr Val Pro Ser Trp Pro Thr Ala Pro Val Pro Ser Ala Gly Glu	
CCC GGG GAG GAG GCG CCC TAT CTG GTG AAG GTG CAC CAG GTG TGG GCG	771
Pro Gly Glu Glu Ala Pro Tyr Leu Val Lys Val His Gln Val Trp Ala	
Lys Val His Glu Val Trp Ala	
GGF-II 01 & GGF-II 11	
GTG AAA GCC GGG GCG TTG AAG AAG GAC TCG CTG CTC ACC GTG GCG CTG	819
Val Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu Leu Thr Val Arg Leu	
Ala Lys	
GGG ACC TGG GGC CAC CCC GCC TTC CCC TCC TGC GGG AGG CTC AAG GAG	867
Gly Thr Trp Gly His Pro Ala Phe Pro Ser Cys Gly Arg Leu Lys Glu	
Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr	
GGF-II 03	
GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAC GCC AAC AGC ACC AGC	915
Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Asp Ala Asn Ser Thr Ser	
Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly	
GGF-II 02	

# FIG. 45C

## Nucleotide Sequence & Deduced Acid Sequence of GGF2HBS5

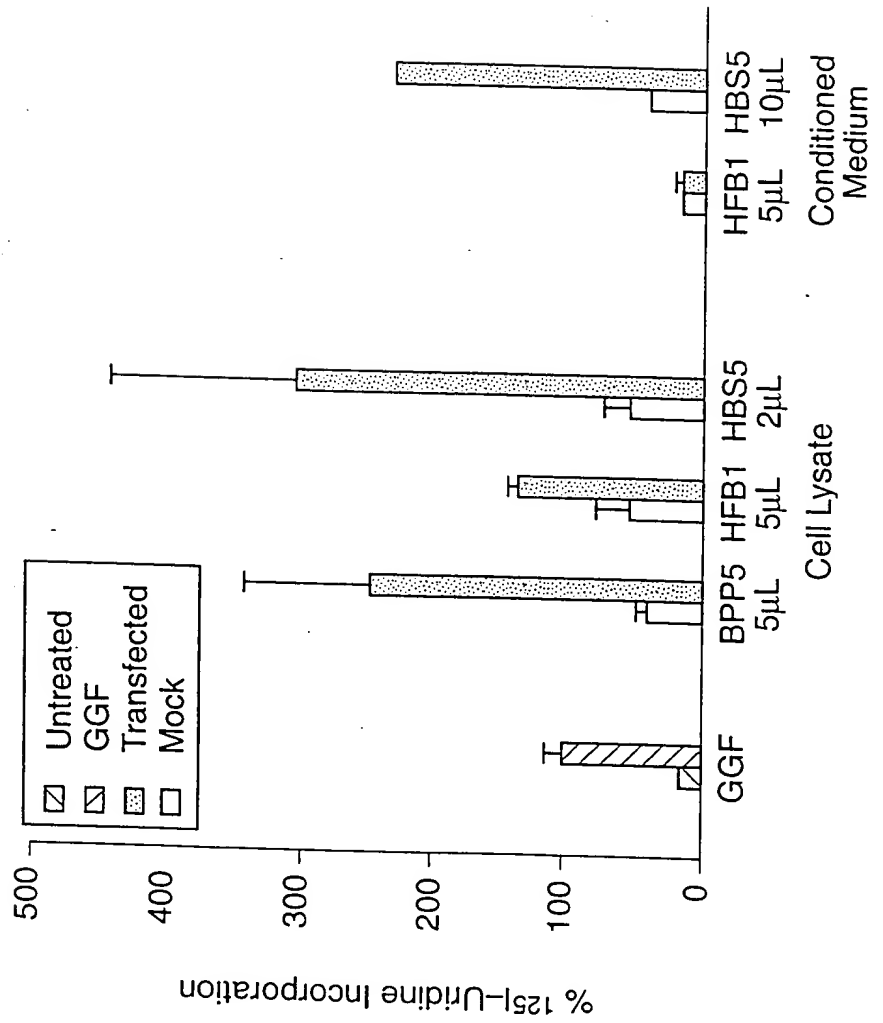
CGC GCG CCG GCC GCC TTC CGA GCC TCT TTC CCC CCT CTG GAG ACG GGC Arg Ala Pro Ala Ala Phe Arg Ala Ser Phe Pro Pro Leu Glu Thr Gly	963
CGG AAC CTC AAG AAG GAG GTC AGC CGG GTG CTG TGC AAG CCG TGC GCC Arg Asn Leu Lys Lys Glu Val Ser Arg Val Leu Cys Lys Arg Cys Ala	1011
TTG CCT CCC CAA TTG AAA GAG ATG AAA AGC CAG GAA TCG GCT GCA GGT Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala Gly	1059
TCC AAA CTA GTC CTT CCG TGT GAA ACC AGT TCT GAA TAC TCC TCT CTC Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Leu Val Leu Arg	1107
GGF-II 06	
AGA TTC AAG TGG TTC AAG AAT GGG AAT GAA TTG AAT CGA AAA AAC AAA Arg Phe Lys Lys Trp Phe Lys Lys Asn Gly Asn Glu Leu Asn Arg Lys Asn Lys	1155
CCA CAA AAT ATC AAG ATA CAA AAA AAG CCA GGG AAG TCA GAA CTT CGC Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg	1203
ATT AAC AAA GCA TCA CTG GCT GAT TCT GGA GAG TAT ATG TGC AAA GTG Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Xaa Lyx	1251
GGF-II 12	
ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT GCC AAT ATC ACC ATC GTG Ile Ser Lys Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val	1299
GAA TCA AAC GCT ACA TCT ACA TCC ACC ACT GGG ACA AGC CAT CTT GTA Glu Ser Asn Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser His Leu Val	1347

# FIG. 45D

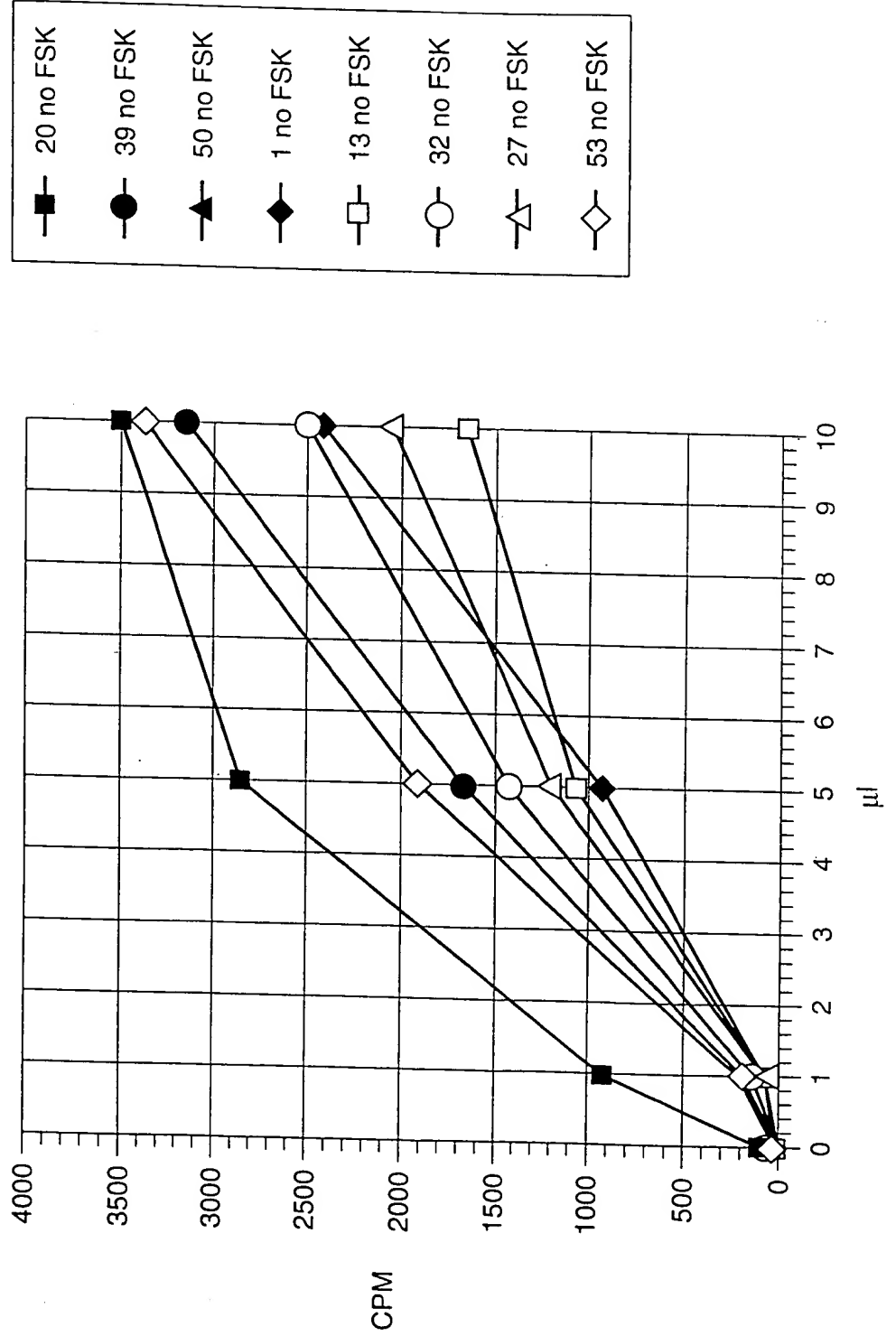
## Nucleotide Sequence & Deduced Acid Sequence of GGF2HBS5

AAA TGT GCG GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGG GAG TGC  
 Lys Cys Ala Glu Lys Lys Glu Thr Phe Cys Val Asn Gly Gly Glu Cys 1395  
  
 TTC ATG GTG AAA GAC CTT TCA AAC CCC TCG AGA TAC TTG TGC AAG TGC  
 Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys 1443  
  
 CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC  
 Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser 1491  
  
 TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA  
 Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu 1530  
  
 TAGGAGCATG CTCAGTTGGT GCTGCTTTCT TGTGTGCTGCA TCTCCCCCTCA GATTCCACCT 1590  
  
 AGAGCTAGAT GTGTCTTACC AGATCTAATA TTGACTGCCT CTGCCTGTCTG CATGAGAACA 1650  
  
 TTAACAAAAAG CAATTGTATT ACTTCCTCTG TTCGCGACTA GTTGGCTCTG AGATACTAAT 1710  
  
 AGGTGTGTGA GGCTCCGGAT GTTTCTGGAA TTGATATTGA ATGATGTGAT ACAAAATTGAT 1770  
  
 AGTCAATATC AAGCAGTGAA ATATGATAAT AAAGGCATTT CAAAGTCTCA CTTTATTGA 1830  
  
 TAAATAAAAA ATCATTCTAC TGAACAGTCC ATCTTCTTTA TACAATGACC ACATCCTGAA 1890  
  
 AAGGGTGTG CTAAGCTGTA ACCGATATGC ACTTGAAATG ATGGTAAAGTT AATTTTGATT 1950  
  
 CAGAATGTGT TATTGTGCAC AAATAAACAT AATAAAAGGA AAAAAA AAA 2003

**FIG. 46**  
Schwann Cell Proliferation Assay



Year	Percentage (%)
1990	65
1991	70
1992	75
1993	75
1994	70
1995	75
1996	80
1997	82
1998	85
1999	90
2000	100



**FIG. 48**  
Schwann Cell Assay/Baculovirus Clones

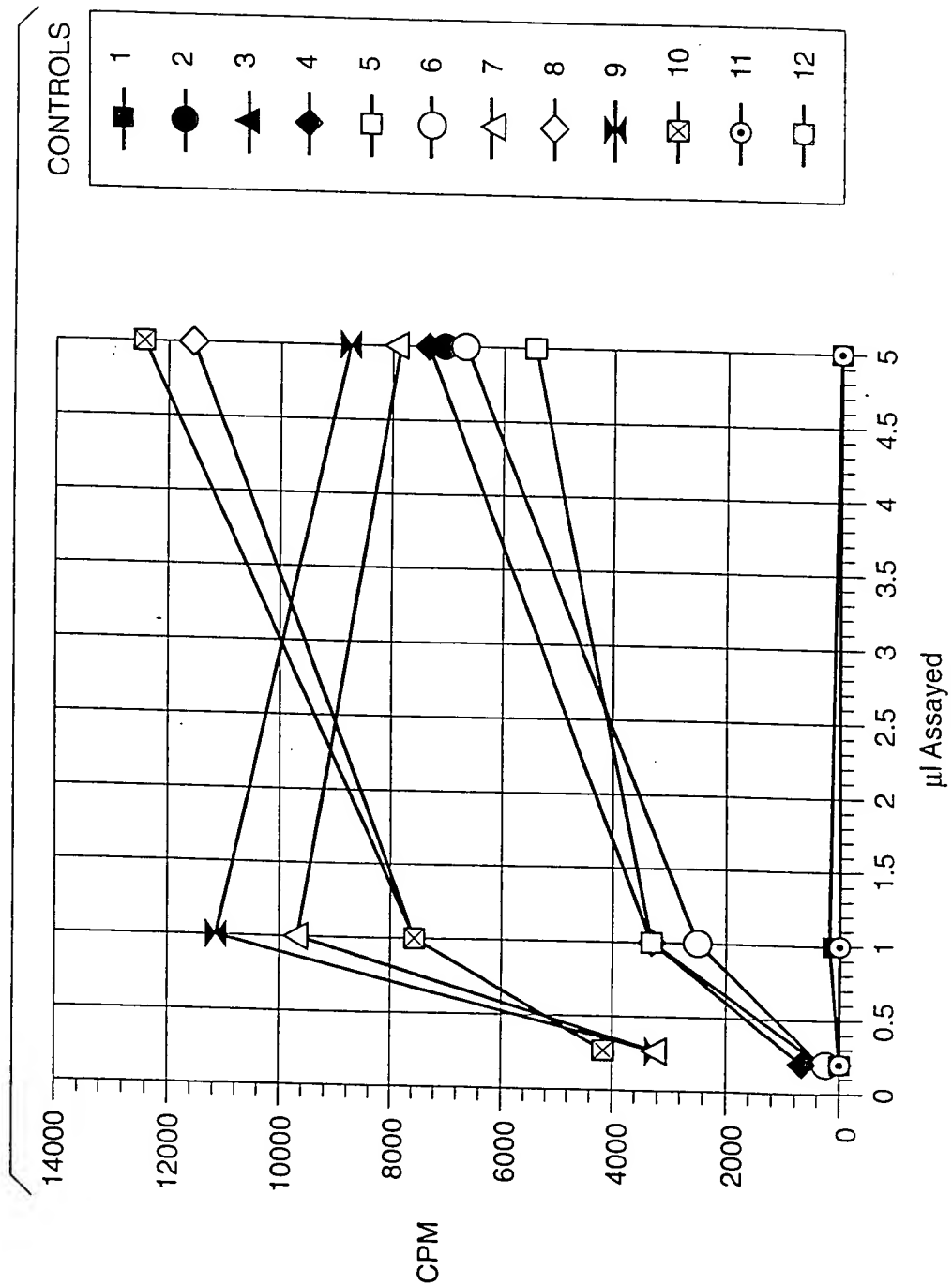


FIG. 49

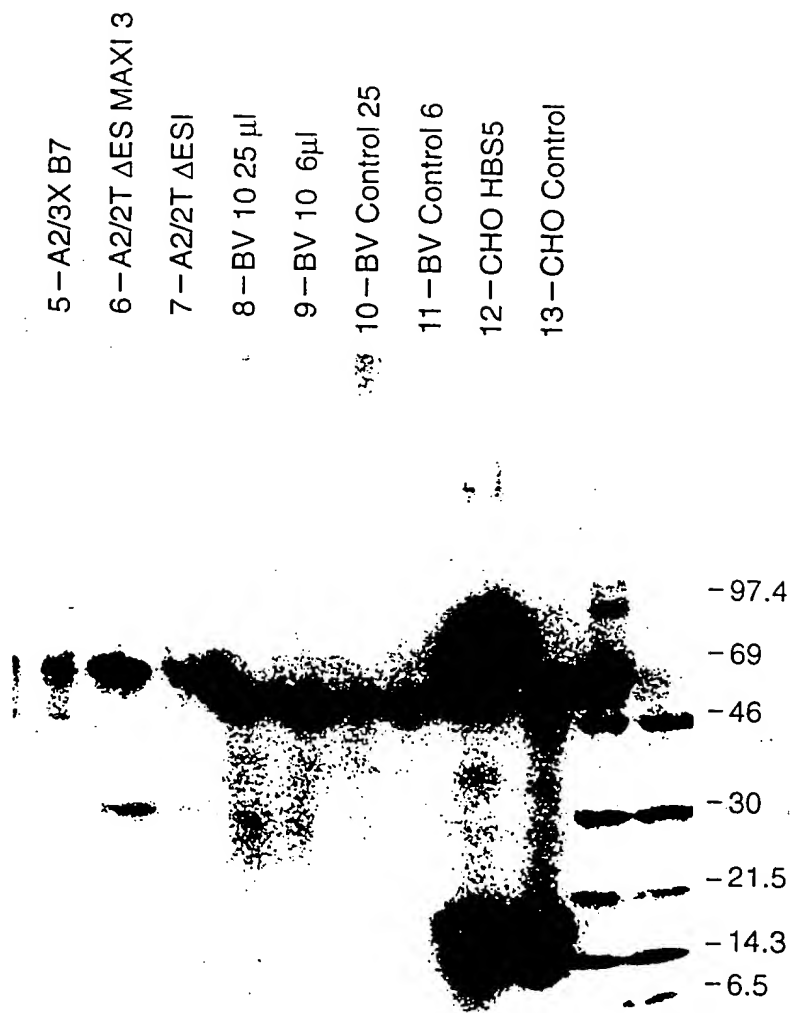


FIG. 50A

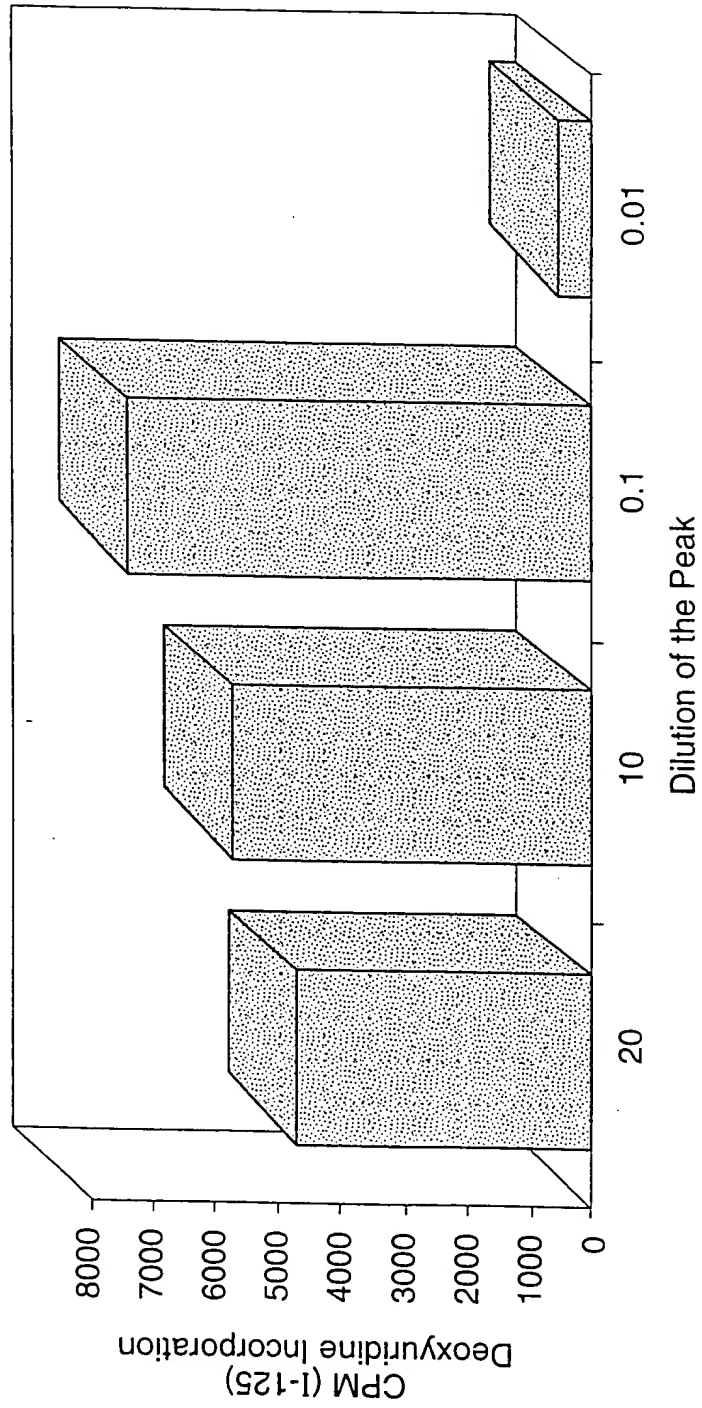
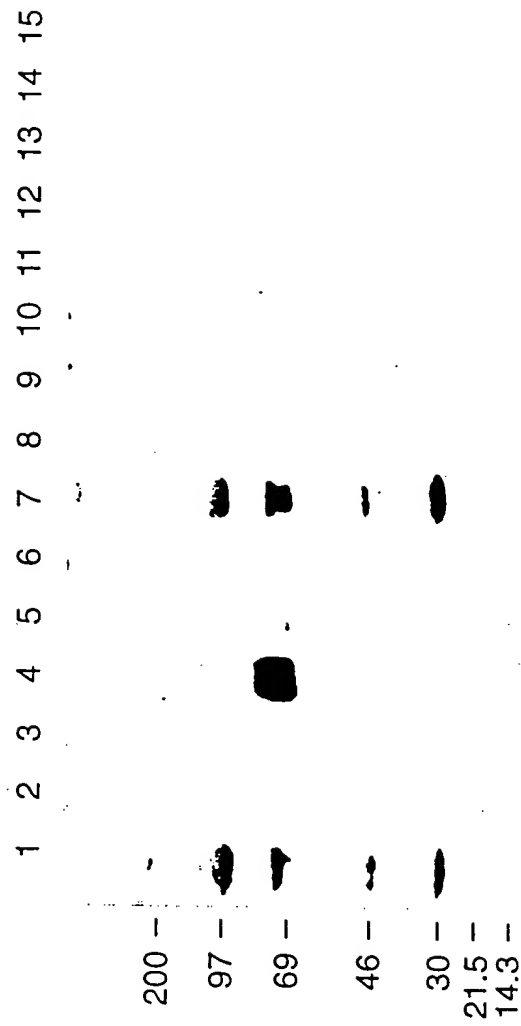
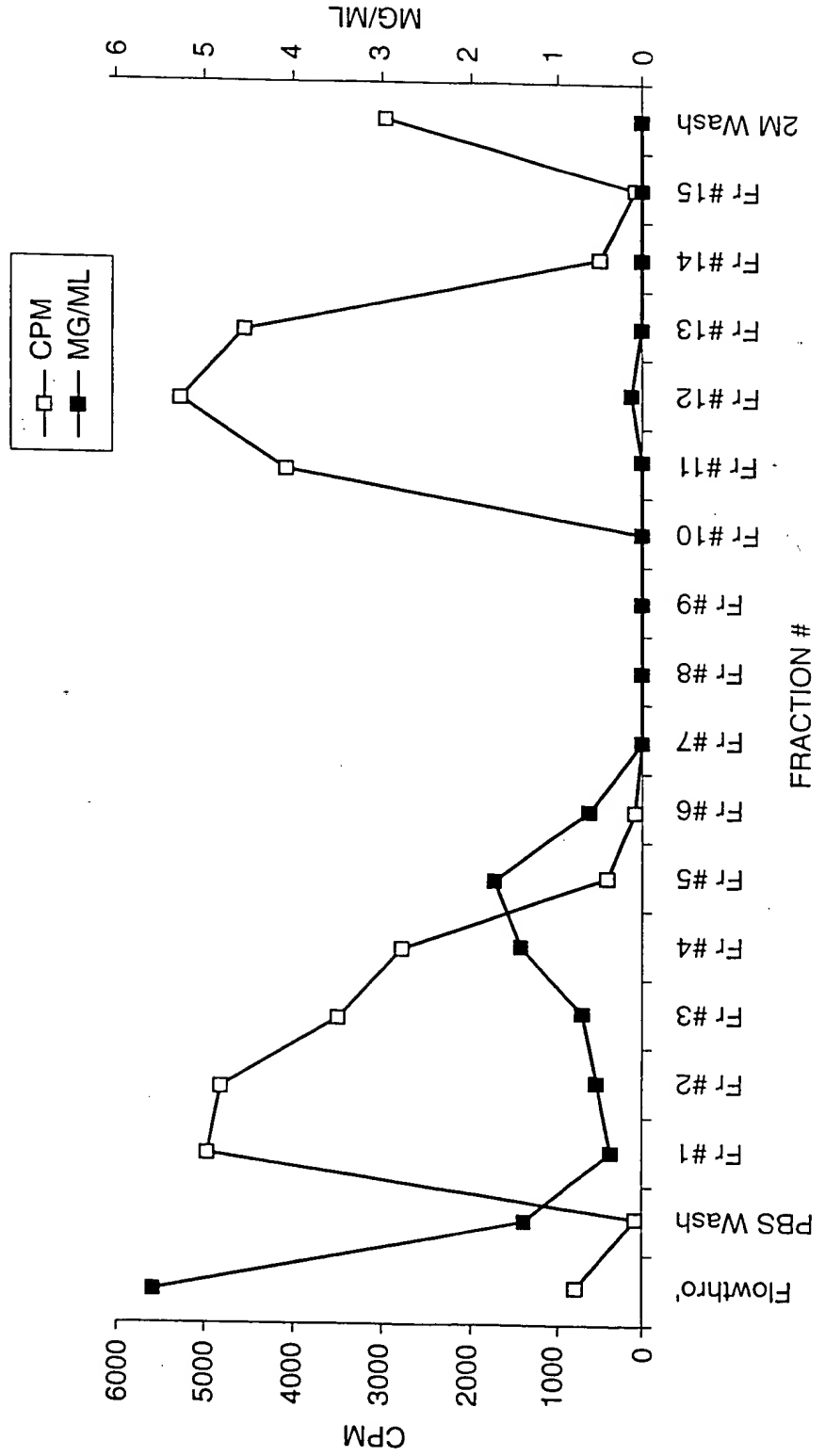




FIG. 50B

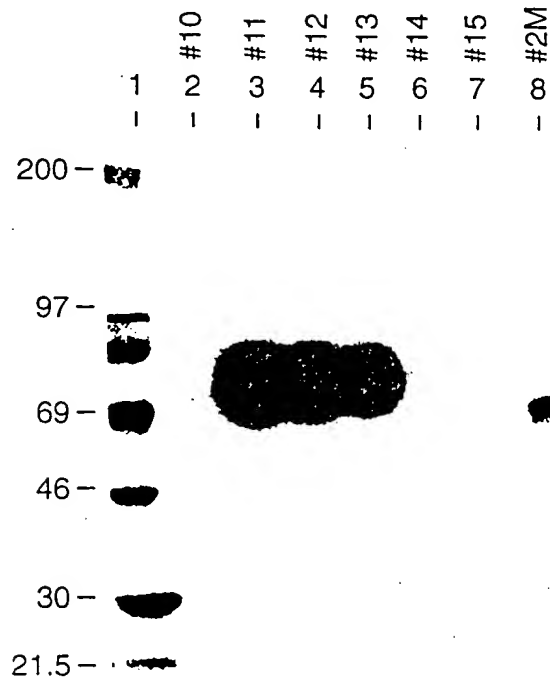
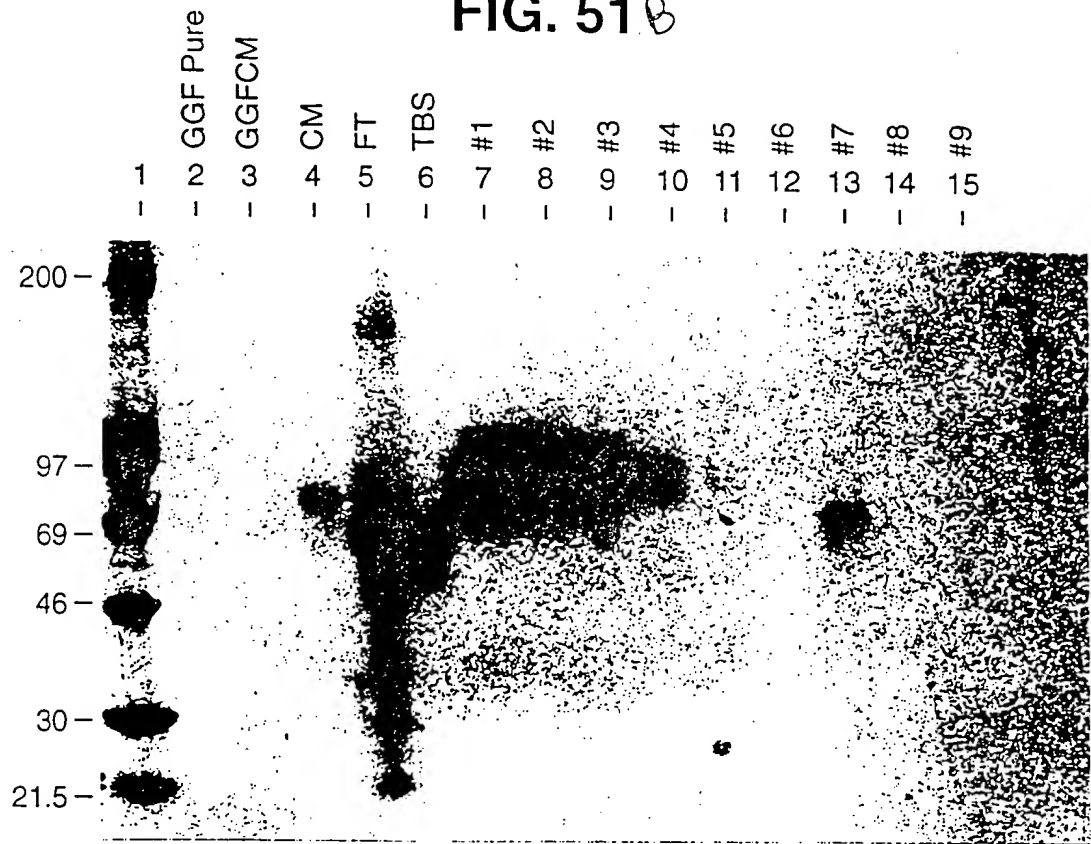


**FIG. 51A**  
rGGF Purification on Cation Exchange Column

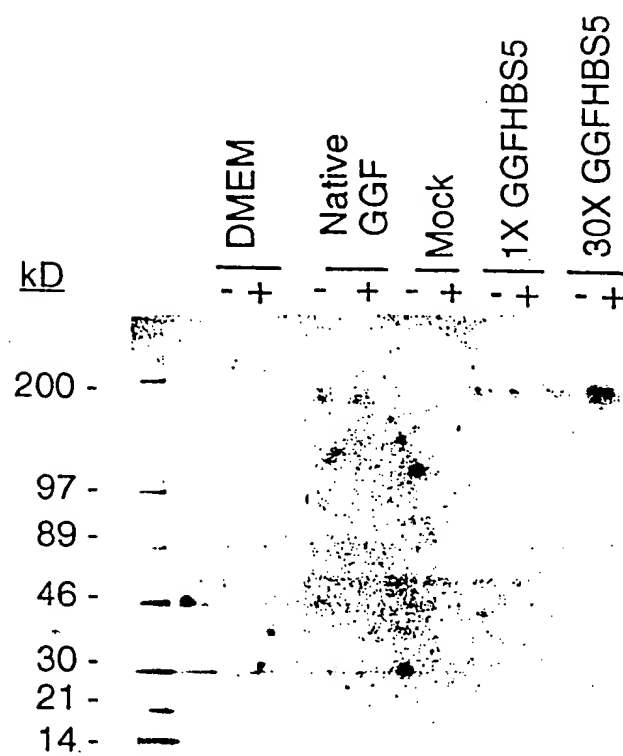


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FIG. 51



**FIG. 52**



**FIG. 53**

# Deduced Sequences of Human & Bovine Glial Growth Factors

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**FIG. 54**